FIG. 1

heart
brain
placenta
lung
liver
skeletal muscle
kidney
pancreas
stomach
thyroid
spinal cord
lymph node
trachea
adrenal gland
bone marrow
spleen
thymus
prostate
testis
ovary
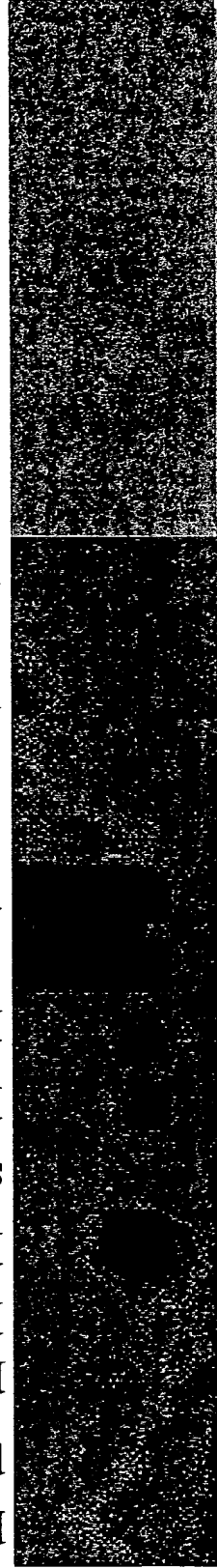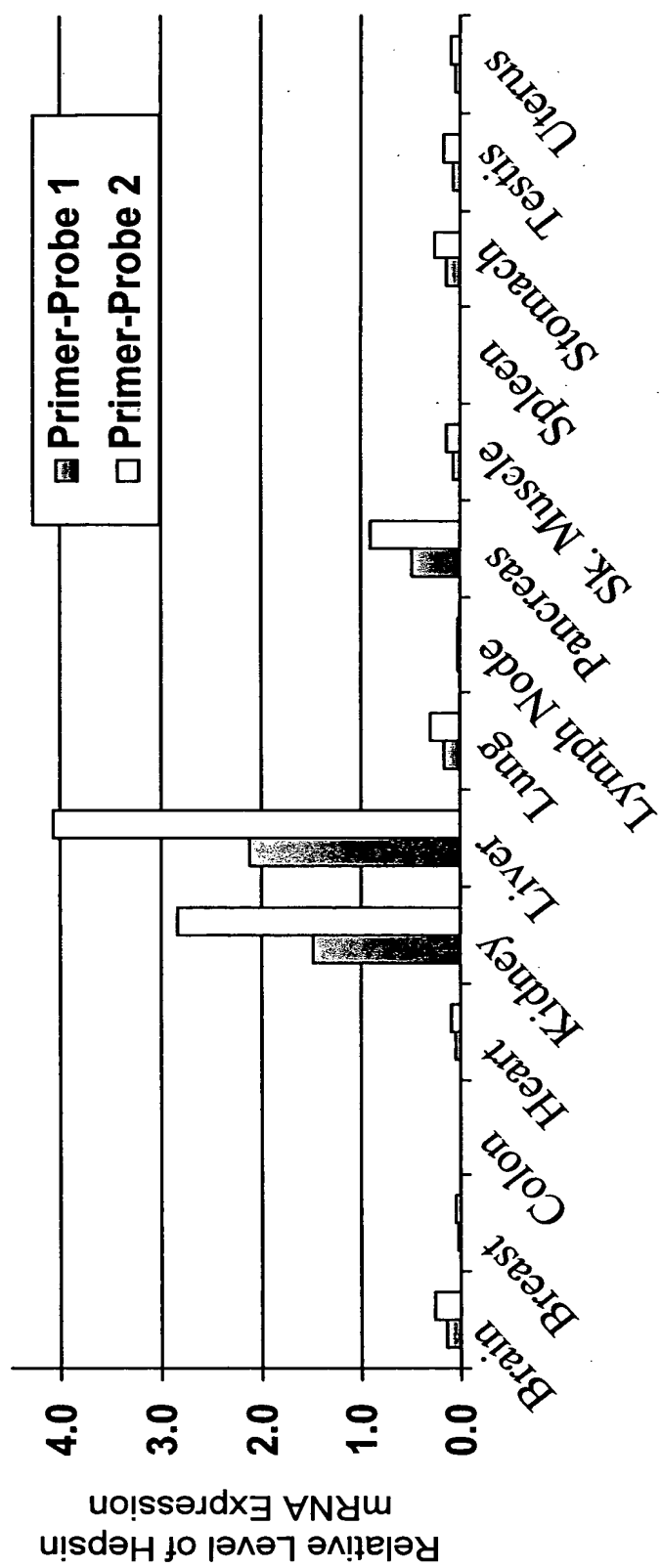small intestine
colon
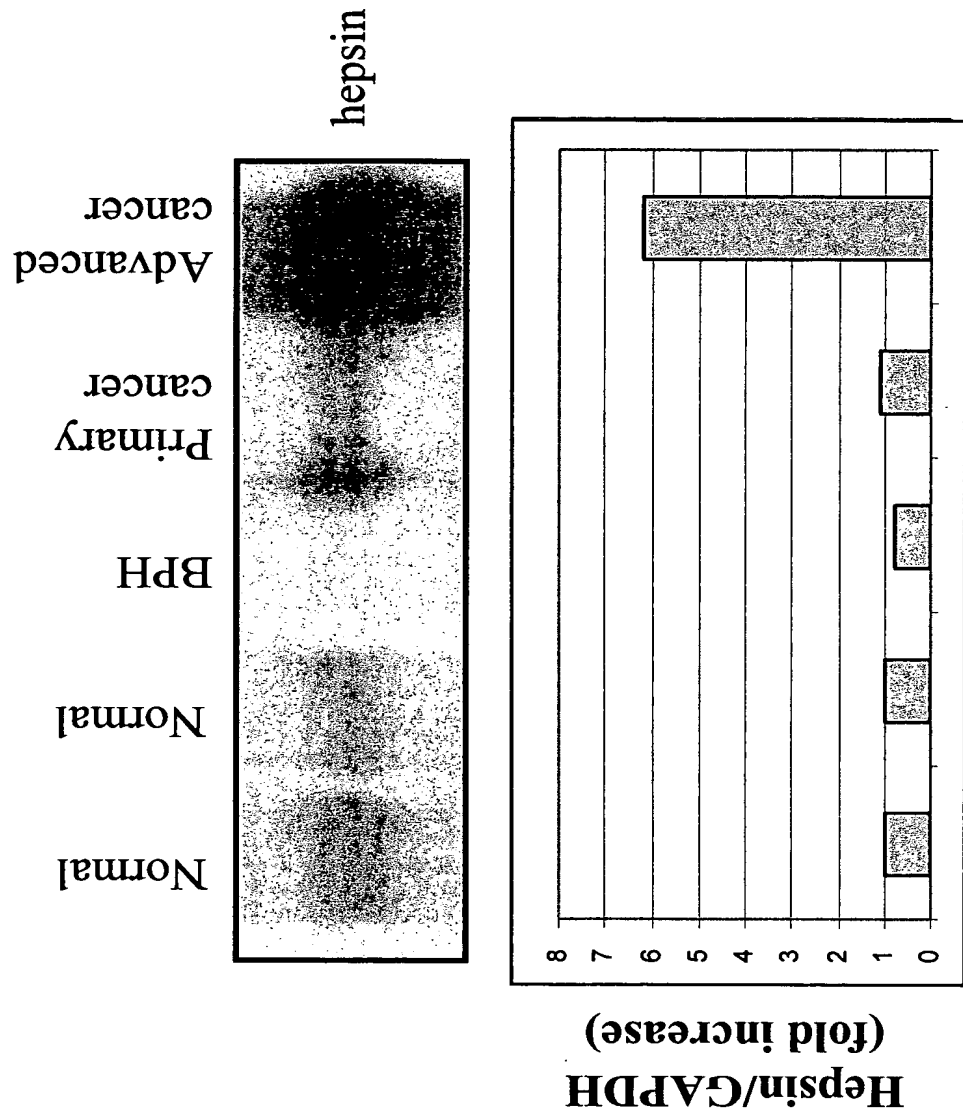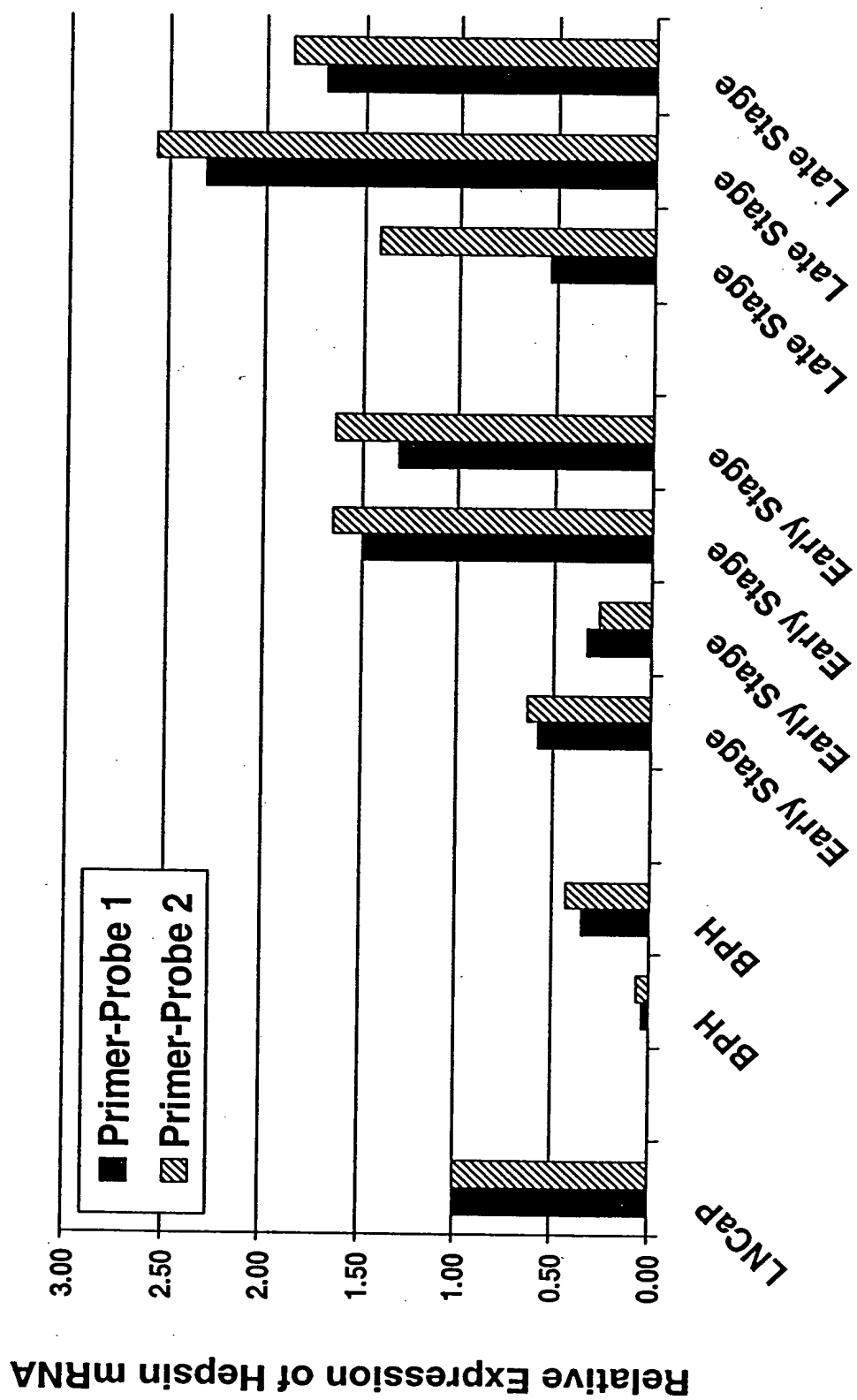peripheral blood leukocyte

FIG. 2

FIG. 3

FIG. 4

Relative Expression of Hepsin mRNA

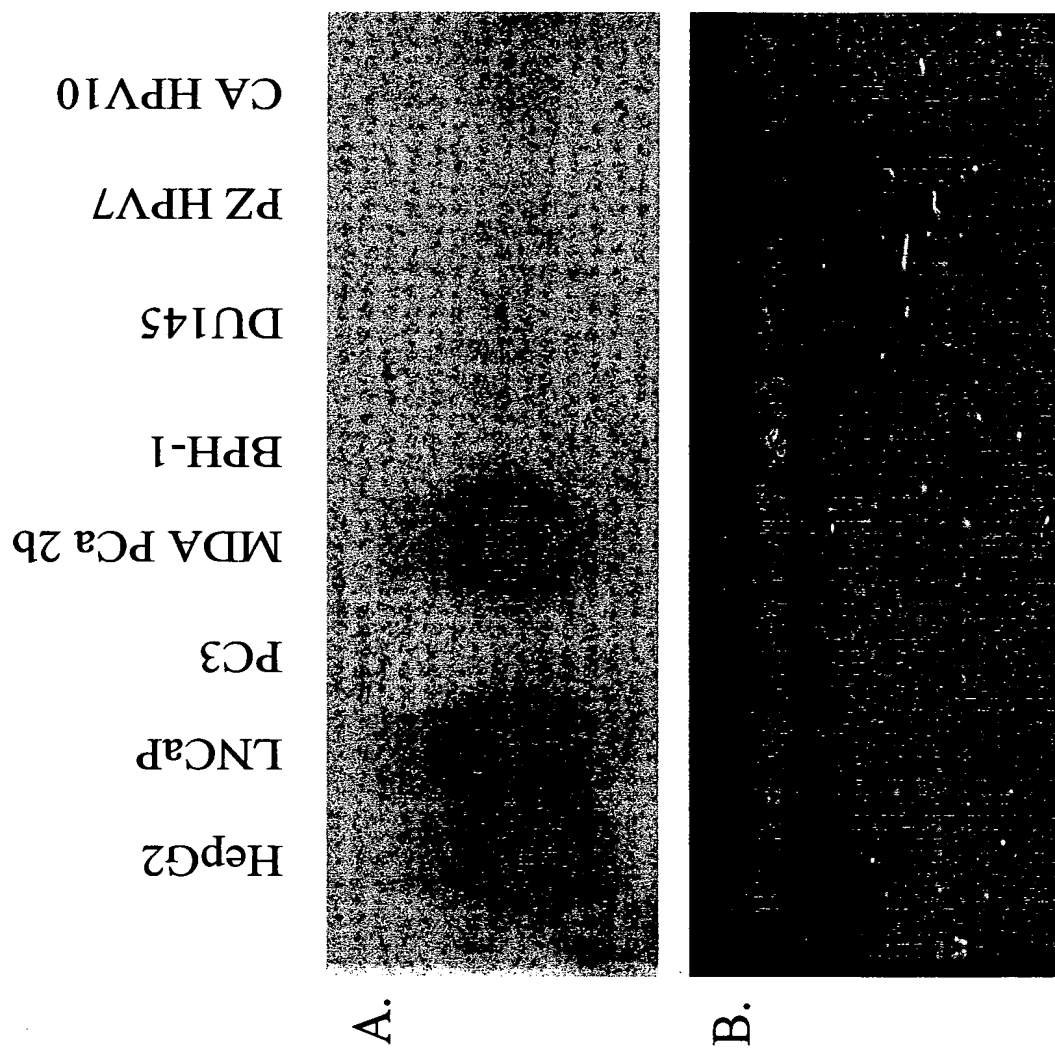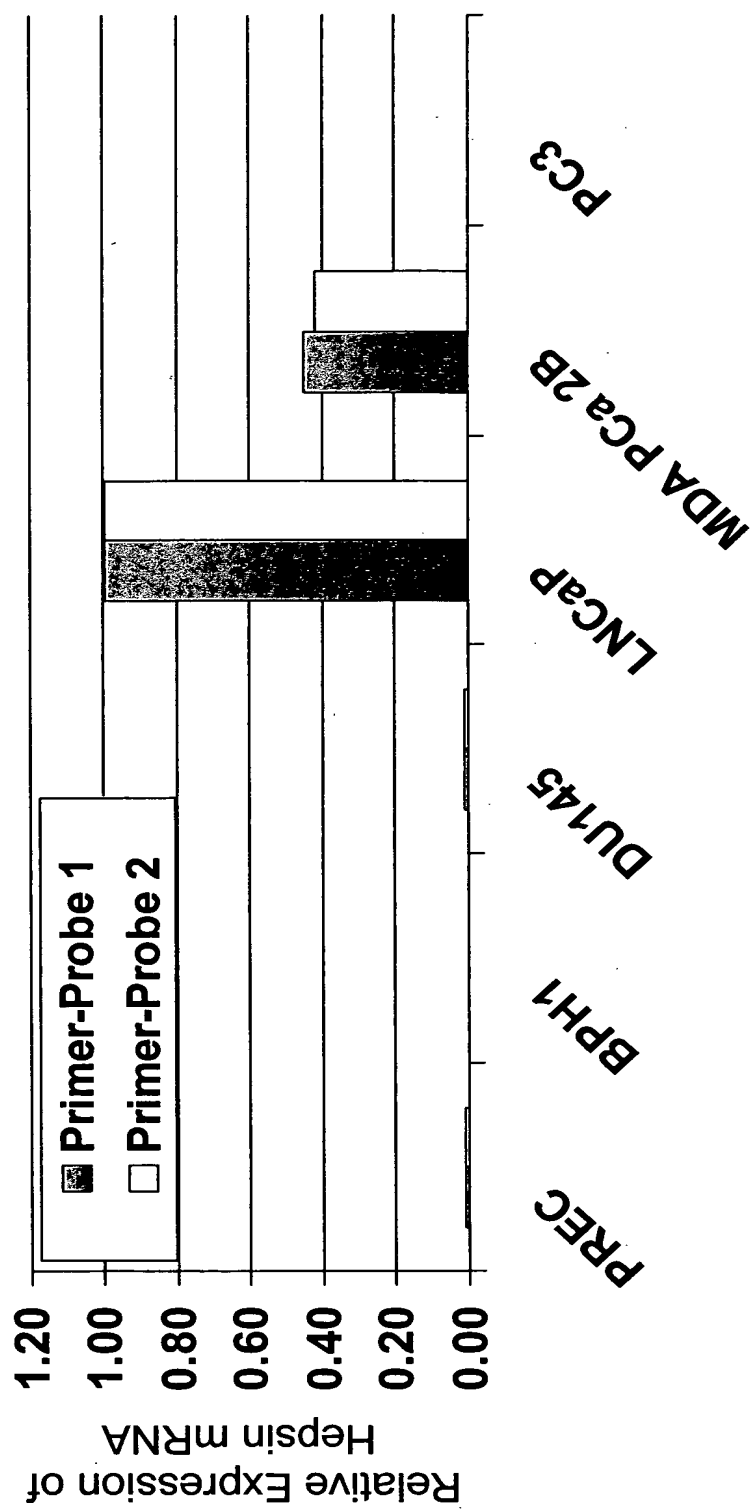Primer-Probe 1
Primer-Probe 2

FIG. 5
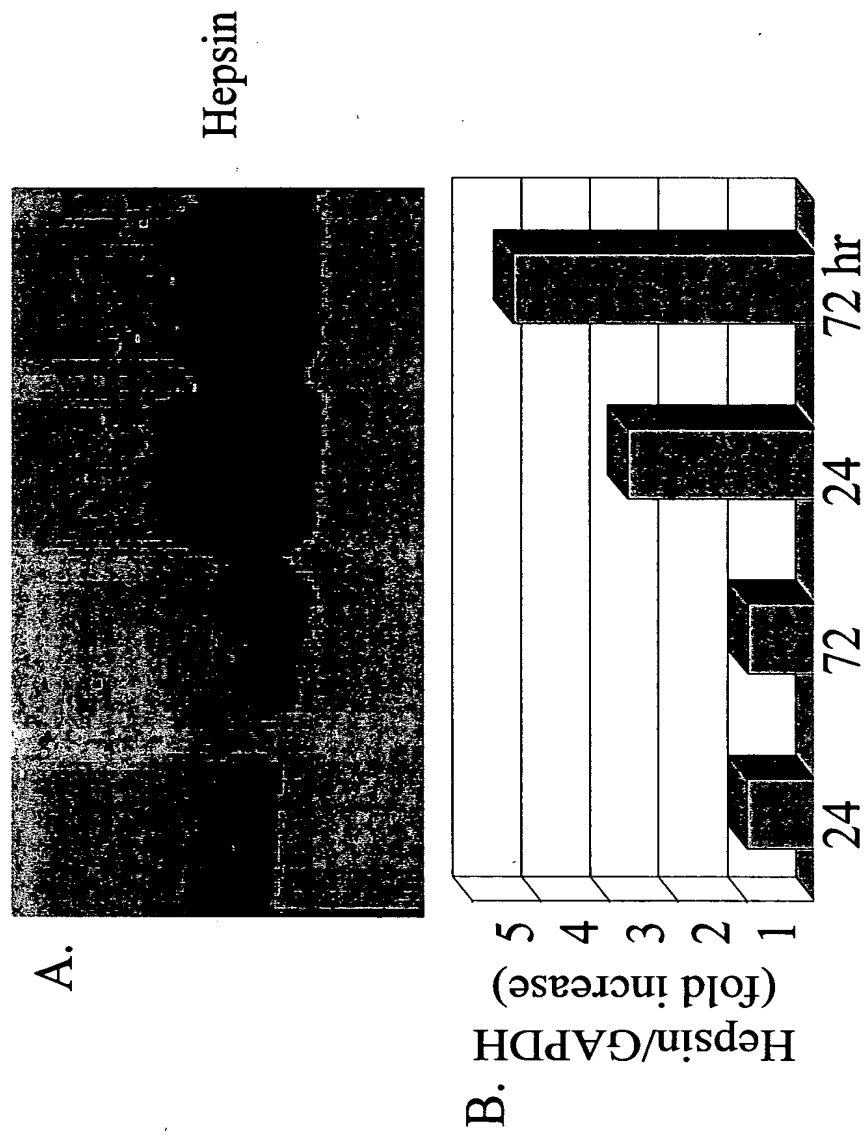
FIG. 6

FIG. 7

FIG. 8

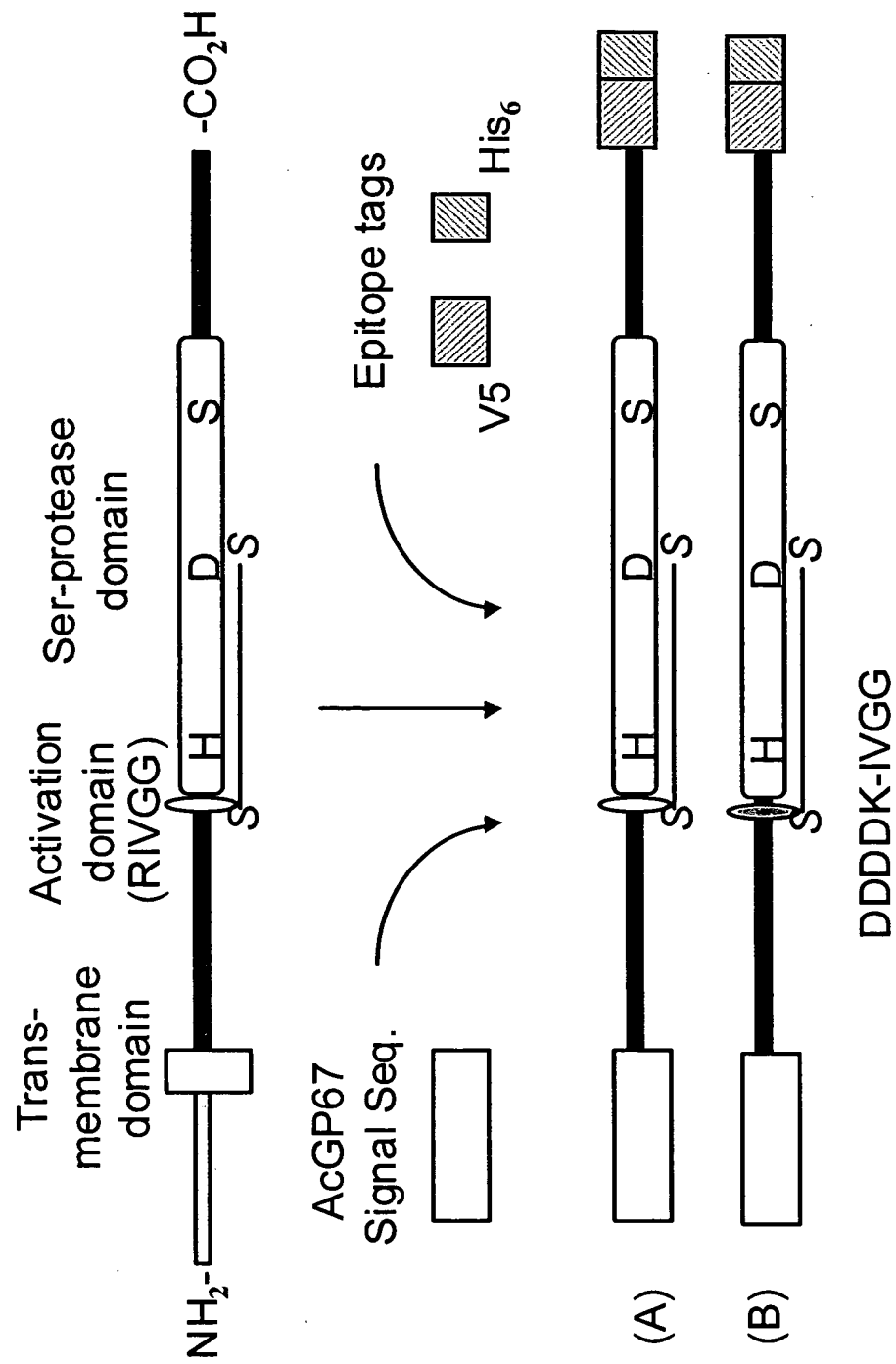# FIG. 9-1

pIRESpuro2W/hepEK_k

```
   1  GACGGATCGG GAGATCTCCC GATCCCCTAT GGTCGACTCT CAGTACAATC
      CTGCCTAGCC CTCTAGAGGG CTAGGGGATA CCAGCTGAGA GTCATGTTAG
  51  TGCTCTGATG CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT
      ACGAGACTAC GGCGTATCAA TTCGGTCATA GACGAGGGAC GAACACACAA
 101  GGAGGTCGCT GAGTAGTGCG CGAGCAAAAT TTAAGCTACA ACAAGGCAAG
      CCTCCAGCGA CTCATCACGC GCTCGTTTTA AATTCGATGT TGTTCCGTTC
 151  GCTTGACCGA CAATTGCATG AAGAATCTGC TTAGGGTTAG GCGTTTTGCG
      CGAACTGGCT GTTAACGTAC TTCTTAGACG AATCCCAATC CGCAAAACGC
 201  CTGCTTCGCG ATGTACGGGC CAGATATACG CGTTGACATT GATTATTGAC
      GACGAAGCGC TACATGCCCG GTCTATATGC GCAACTGTAA CTAATAACTG
 251  TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA
      ATCAATAATT ATCATTAGTT AATGCCCCAG TAATCAAGTA TCGGGTATAT
 301  TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG
      ACCTCAAGGC GCAATGTATT GAATGCCATT TACCGGGCGG ACCGACTGGC
 351  CCCAACGACC CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT
      GGGTTGCTGG GGGCGGGTAA CTGCAGTTAT TACTGCATAC AAGGGTATCA
 401  AACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAC TATTTACGGT
      TTGCGGTTAT CCCTGAAAGG TAACTGCAGT TACCCACCTG ATAAATGCCA
 451  AAACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCCC
      TTTGACGGGT GAACCGTCAT GTAGTTCACA TAGTATACGG TTCATGCGGG
 501  CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT ATGCCCAGTA
      GGATAACTGC AGTTACTGCC ATTTACCGGG CGGACCGTAA TACGGGTCAT
 551  CATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA
      GTACTGGAAT ACCCTGAAAG GATGAACCGT CATGTAGATG CATAATCAGT
 601  TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA
      AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT ACCCGCACCT
 651  TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
      ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT
 701  TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA
      ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT
 751  ACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG
      TGTTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC
 801  GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
      CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTTGGGT GACGAATGAC
 851  GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTTGGTACC
      CGAATAGCTT TAATTATGCT GAGTGATATC CCTCTGGGTT CGAACCATGG
  +3                                  M  E  T  D  T  L  L  W
 901  GAGCTCGGAT CGATATCGCC ACCATGGAGA CAGACACACT CCTGCTATGG
      CTCGAGCCTA GCTATAGCGG TGGTACCTCT GTCTGTGTGA GGACGATACC
  +3   V  L  L  L  W  V  P  G  S  T  G  D  A  P  D  R  S·
 951  GTACTGCTGC TCTGGGTTCC AGGTTCCACT GGTGACGCTC CGGACAGGAG
      CATGACGACG AGACCCAAGG TCCAAGGTGA CCACTGCGAG GCCTGTCCTC
  +3  ·S  D  Q  E  P  L  Y  P  V  Q  V  S  S  A  D  A  R  L
1001  TGACCAGGAG CCGCTGTACC CAGTGCAGGT CAGCTCTGCG GACGCTCGGC
      ACTGGTCCTC GGCGACATGG GTCACGTCCA GTCGAGACGC CTGCGAGCCG
```

FIG. 9-2

pIRESpuro2W/hepEK_k

```
+3    ·L  M  V  F  D  K  T  E  G  T  W  R  L  L  C  S  S
1051  TCATGGTCTT TGACAAGACG GAAGGGACGT GGCGGCTGCT GTGCTCCTCG
      AGTACCAGAA ACTGTTCTGC CTTCCCTGCA CCGCCGACGA CACGAGGAGC

+3     R  S  N  A  R  V  A  G  L  S  C  E  E  M  G  F  L·
1101  CGCTCTAACG CCAGGGTAGC CGGACTCAGC TGCGAGGAGA TGGGCTTCCT
      GCGAGATTGC GGTCCCATCG GCCTGAGTCG ACGCTCCTCT ACCCGAAGGA

+3    ·L  R  A  L  T  H  S  E  L  D  V  R  T  A  G  A  N  G
1151  CAGGGCACTG ACCCACTCCG AGCTGGACGT GCGAACGGCG GGCGCCAATG
      GTCCCGTGAC TGGGTGAGGC TCGACCTGCA CGCTTGCCGC CCGCGGTTAC

+3    ·G  T  S  G  F  F  C  V  D  E  G  R  L  P  H  T  Q
1201  GCACGTCGGG CTTCTTCTGT GTGGACGAGG GGAGGCTGCC CCACACCCAG
      CGTGCAGCCC GAAGAAGACA CACCTGCTCC CCTCCGACGG GGTGTGGGTC

+3     R  L  L  E  V  I  S  V  C  D  C  P  R  G  R  F  L·
1251  AGGCTGCTGG AGGTCATCTC CGTGTGTGAT TGCCCCAGAG CCGTTTCTT
      TCCGACGACC TCCAGTAGAG GCACACACTA ACGGGGTCTC CGGCAAAGAA

+3    ·L  A  A  I  C  Q  D  C  G  R  R  K  L  P  V  D  D  D
1301  GGCCGCCATC TGCCAAGACT GTGGCCGCAG GAAGCTGCCC GTGGACGACG
      CCGGCGGTAG ACGGTTCTGA CACCGGCGTC CTTCGACGGG CACCTGCTGC

+3    ·D  D  K  I  V  G  R  D  T  S  L  G  R  W  P  W
1351  ACGACAAGAT CGTGGGAGGC CGGGACACCA GCTTGGGCCG GTGGCCGTGG
      TGCTGTTCTA GCACCCTCCG GCCCTGTGGT CGAACCCGGC CACCGGCACC

+3     Q  V  S  L  R  Y  D  G  A  H  L  C  G  G  S  L  L·
1401  CAAGTCAGCC TTCGCTATGA TGGAGCACAC CTCTGTGGGG GATCCCTGCT
      GTTCAGTCGG AAGCGATACT ACCTCGTGTG GAGACACCCC CTAGGGACGA

+3    ·L  S  G  D  W  V  L  T  A  A  H  C  F  P  E  R  N  R
1451  CTCCGGGGAC TGGGTGCTGA CAGCCGCCCA CTGCTTCCCG GAGCGGAACC
      GAGGCCCCTG ACCCACGACT GTCGGCGGGT GACGAAGGGC CTCGCCTTGG

+3    ·R  V  L  S  R  W  R  V  F  A  G  A  V  A  Q  A  S
1501  GGGTCCTGTC CCGATGGCGA GTGTTTGCCG GTGCCGTGGC CCAGGCCTCT
      CCCAGGACAG GGCTACCGCT CACAAACGGC CACGGCACCG GGTCCGGAGA

+3     P  H  G  L  Q  L  G  V  Q  A  V  V  Y  H  G  G  Y·
1551  CCCCACGGTC TGCAGCTGGG GGTGCAGGCT GTGGTCTACC ACGGGGGCTA
      GGGGTGCCAG ACGTCGACCC CCACGTCCGA CACCAGATGG TGCCCCCGAT

+3    ·Y  L  P  F  R  D  P  N  S  E  E  N  S  N  D  I  A  L
1601  TCTTCCCTTT CGGGACCCCA ACAGCGAGGA GAACAGCAAC GATATTGCCC
      AGAAGGGAAA GCCCTGGGGT TGTCGCTCCT CTTGTCGTTG CTATAACGGG

+3    ·L  V  H  L  S  S  P  L  P  L  T  E  Y  I  Q  P  V
1651  TGGTCCACCT CTCCAGTCCC CTGCCCCTCA CAGAATACAT CCAGCCTGTG
      ACCAGGTGGA GAGGTCAGGG GACGGGGAGT GTCTTATGTA GGTCGGACAC

+3     C  L  P  A  A  G  Q  A  L  V  D  G  K  I  C  T  V·
1701  TGCCTCCCAG CTGCCGGCCA GGCCCTGGTG GATGGCAAGA TCTGTACCGT
      ACGGAGGGTC GACGGCCGGT CCGGGACCAC CTACCGTTCT AGACATGGCA

+3    ·V  T  G  W  G  N  T  Q  Y  Y  G  Q  Q  A  G  V  L  Q
1751  GACGGGCTGG GGCAACACGC AGTACTATGG CCAACAGGCC GGGGTACTCC
      CTGCCCGACC CCGTTGTGCG TCATGATACC GGTTGTCCGG CCCCATGAGG
```

II/51

FIG. 9-3

pIRESpuro2W/hepEK_k

```
+3   ·Q  E  A  R  V  P  I  I  S  N  D  V  C  N  G  A  D
1801  AGGAGGCTCG AGTCCCCATA ATCAGCAATG ATGTCTGCAA TGGCGCTGAT .
      TCCTCCGAGC TCAGGGGTAT TAGTCGTTAC TACAGACGTT ACCGCGACTA
+3    F  Y  G  N  Q  I  K  P  K  M  F  C  A  G  Y  P  E·
1851  TTCTATGGAA ACCAGATCAA GCCCAAGATG TTCTGTGCTG GCTACCCCGA
      AAGATACCTT TGGTCTAGTT CGGGTTCTAC AAGACACGAC CGATGGGGCT
+3    ·E  G  G  I  D  A  C  Q  G  D  S  G  G  P  F  V  C  E
1901  GGGTGGCATT GATGCCTGCC AGGGCGACAG CGGTGGTCCC TTTGTGTGTG
      CCCACCGTAA CTACGGACGG TCCCGCTGTC GCCACCAGGG AAACACACAC
+3    ·E  D  S  I  S  R  T  P  R  W  R  L  C  G  I  V  S
1951  AGGACAGCAT CTCTCGGACG CCACGTTGGC GGCTGTGTGG CATTGTGAGT
      TCCTGTCGTA GAGAGCCTGC GGTGCAACCG CCGACACACC GTAACACTCA
+3    W  G  T  G  C  A  L  A  Q  K  P  G  V  Y  T  K  V·
2001  TGGGGCACTG GCTGTGCCCT GGCCCAGAAG CCAGGCGTCT ACACCAAAGT
      ACCCCGTGAC CGACACGGGA CCGGGTCTTC GGTCCGCAGA TGTGGTTTCA
+3    ·V  S  D  F  R  E  W  I  F  Q  A  I  K  T  H  S  E  A·
2051  CAGTGACTTC CGGGAGTGGA TCTTCCAGGC CATAAAGACT CACTCCGAAG
      GTCACTGAAG GCCCTCACCT AGAAGGTCCG GTATTTCTGA GTGAGGCTTC
+3    ·A  S  G  M  V  T  Q  L  E  F  G  K  P  I  P  N  P
2101  CCAGCGGCAT GGTGACCCAG CTCGAATTCG GTAAGCCTAT CCCTAACCCT
      GGTCGCCGTA CCACTGGGTC GAGCTTAAGC CATTCGGATA GGGATTGGGA
+3    L  L  G  L  D  S  T  R  T  G  H  H  H  H  H  H
2151  CTCCTCGGTC TCGATTCTAC GCGTACCGGT CATCATCACC ATCACCATTG
      GAGGAGCCAG AGCTAAGATG CGCATGGCCA GTAGTAGTGG TAGTGGTAAC
2201  AGTTTAAAGC GGCCGCATAG ATAACTGATC CAGTGTGCTG GAATTAATTC
      TCAAATTTCG CCGGCGTATC TATTGACTAG GTCACACGAC CTTAATTAAG
2251  GCTGTCTGCG AGGGCCAGCT GTTGGGGTGA GTACTCCCTC TCAAAAGCGG
      CGACAGACGC TCCCGGTCGA CAACCCCACT CATGAGGGAG AGTTTTCGCC
2301  GCATGACTTC TGCGCTAAGA TTGTCAGTTT CCAAAAACGA GGAGGATTTG
      CGTACTGAAG ACGCGATTCT AACAGTCAAA GGTTTTTGCT CCTCCTAAAC
2351  ATATTCACCT GGCCCGCGGT GATGCCTTTG AGGGTGGCCG CGTCCATCTG
      TATAAGTGGA CCGGGCGCCA CTACGGAAAC TCCCACCGGC GCAGGTAGAC
2401  GTCAGAAAAG ACAATCTTTT TGTTGTCAAG CTTGAGGTGT GGCAGGCTTG
      CAGTCTTTTC TGTTAGAAAA ACAACAGTTC GAACTCCACA CCGTCCGAAC
2451  AGATCTGGCC ATACACTTGA GTGACAATGA CATCCACTTT GCCTTTCTCT
      TCTAGACCGG TATGTGAACT CACTGTTACT GTAGGTGAAA CGGAAAGAGA
2501  CCACAGGTGT CCACTCCCAG GTCCAACTGC AGGTCGAGCA TGCATCTAGG
      GGTGTCCACA GGTGAGGGTC CAGGTTGACG TCCAGCTCGT ACGTAGATCC
2551  GCGGCCAATT CCGCCCCTCT CCCTCCCCCC CCCTAACGT TACTGGCCGA
      CGCCGGTTAA GGCGGGGAGA GGGAGGGGGG GGGATTGCA ATGACCGGCT
2601  AGCCGCTTGG AATAAGGCCG GTGTGCGTTT GTCTATATGT GATTTTCCAC
      TCGGCGAACC TTATTCCGGC CACACGCAAA CAGATATACA CTAAAAGGTG
2651  CATATTGCCG TCTTTTGGCA ATGTGAGGGC CCGGAAACCT GGCCCTGTCT
      GTATAACGGC AGAAAACCGT TACACTCCCG GGCCTTTGGA CCGGGACAGA
2701  TCTTGACGAG CATTCCTAGG GGTCTTTCCC CTCTCGCCAA AGGAATGCAA
      AGAACTGCTC GTAAGGATCC CCAGAAAGGG GAGAGCGGTT TCCTTACGTT
```

FIG.9-4

pIRESpuro2W/hepEK_k

```
2751    GGTCTGTTGA ATGTCGTGAA GGAAGCAGTT CCTCTGGAAG CTTCTTGAAG
        CCAGACAACT TACAGCACTT CCTTCGTCAA GGAGACCTTC GAAGAACTTC
2801    ACAAACAACG TCTGTAGCGA CCCTTTGCAG GCAGCGGAAC CCCCCACCTG
        TGTTTGTTGC AGACATCGCT GGGAAACGTC CGTCGCCTTG GGGGGTGGAC
2851    GCGACAGGTG CCTCTGCGGC CAAAAGCCAC GTGTATAAGA TACACCTGCA
        CGCTGTCCAC GGAGACGCCG GTTTTCGGTG CACATATTCT ATGTGGACGT
2901    AAGGCGGCAC AACCCCAGTG CCACGTTGTG AGTTGGATAG TTGTGGAAAG
        TTCCGCCGTG TTGGGGTCAC GGTGCAACAC TCAACCTATC AACACCTTTC
2951    AGTCAAATGG CTCTCCTCAA GCGTATTCAA CAAGGGGCTG AAGGATGCCC
        TCAGTTTACC GAGAGGAGTT CGCATAAGTT GTTCCCCGAC TTCCTACGGG
3001    AGAAGGTACC CCATTGTATG GGATCTGATC TGGGGCCTCG GTGCACATGC
        TCTTCCATGG GGTAACATAC CCTAGACTAG ACCCCGGAGC CACGTGTACG
3051    TTTACATGTG TTTAGTCGAG GTTAAAAAAA CGTCTAGGCC CCCCGAACCA
        AAATGTACAC AAATCAGCTC CAATTTTTTT GCAGATCCGG GGGGCTTGGT
3101    CGGGGACGTG GTTTTCCTTT GAAAAACACG ATGATAAGCT TGCCACAACC
        GCCCCTGCAC CAAAAGGAAA CTTTTTGTGC TACTATTCGA ACGGTGTTGG
3151    CACAAGGAGA CGACCTTCCA TGACCGAGTA CAAGCCCACG GTGCGCCTCG
        GTGTTCCTCT GCTGGAAGGT ACTGGCTCAT GTTCGGGTGC CACGCGGAGC
3201    CCACCCGCGA CGACGTCCCC CGGGCCGTAC GCACCCTCGC CGCCGCGTTC
        GGTGGGCGCT GCTGCAGGGG GCCCGGCATG CGTGGGAGCG GCGGCGCAAG
3251    GCCGACTACC CCGCCACGCG CCACACCGTC GACCCGGACC GCCACATCGA
        CGGCTGATGG GGCGGTGCGC GGTGTGGCAG CTGGGCCTGG CGGTGTAGCT
3301    GCGGGTCACC GAGCTGCAAG AACTCTTCCT CACGCGCGTC GGGCTCGACA
        CGCCCAGTGG CTCGACGTTC TTGAGAAGGA GTGCGCGCAG CCCGAGCTGT
3351    TCGGCAAGGT GTGGGTCGCG GACGACGGCG CCGCGGTGGC GGTCTGGACC
        AGCCGTTCCA CACCCAGCGC CTGCTGCCGC GGCGCCACCG CCAGACCTGG
3401    ACGCCGGAGA GCGTCGAAGC GGGGGCGGTG TTCGCCGAGA TCGGCCCGCG
        TGCGGCCTCT CGCAGCTTCG CCCCCGCCAC AAGCGGCTCT AGCCGGGCGC
3451    CATGGCCGAG TTGAGCGGTT CCCGGCTGGC CGCGCAGCAA CAGATGGAAG
        GTACCGGCTC AACTCGCCAA GGGCCGACCG GCGCGTCGTT GTCTACCTTC
3501    GCCTCCTGGC GCCGCACCGG CCCAAGGAGC CGCGTGGTT CCTGGCCACC
        CGGAGGACCG CGGCGTGGCC GGGTTCCTCG GCGCACCAA GGACCGGTGG
3551    GTCGGCGTCT CGCCCGACCA CCAGGGCAAG GGTCTGGGCA GCGCCGTCGT
        CAGCCGCAGA GCGGGCTGGT GGTCCCGTTC CCAGACCCGT CGCGGCAGCA
3601    GCTCCCCGGA GTGGAGGCGG CCGAGCGCGC CGGGGTGCCC GCCTTCCTGG
        CGAGGGGCCT CACCTCCGCC GGCTCGCGCG GCCCCACGGG CGGAAGGACC
3651    AGACCTCCGC GCCCCGCAAC CTCCCCTTCT ACGAGCGGCT CGGCTTCACC
        TCTGGAGGCG CGGGGCGTTG GAGGGGAAGA TGCTCGCCGA GCCGAAGTGG
3701    GTCACCGCCG ACGTCGAGTG CCCGAAGGAC CGCGCGACCT GGTGCATGAC
        CAGTGGCGGC TGCAGCTCAC GGGCTTCCTG GCGCGCTGGA CCACGTACTG
3751    CCGCAAGCCC GGTGCCTGAC GCCCGCCCCA CGACCCGCAG CGCCCGACCG
        GGCGTTCGGG CCACGGACTG CGGGCGGGGT GCTGGGCGTC GCGGGCTGGC
3801    AAAGGAGCGC ACGACCCCAT GGCTCCGACC GAAGCCGACC CGGGCGGCCC
        TTTCCTCGCG TGCTGGGGTA CCGAGGCTGG CTTCGGCTGG GCCCGCCGGG
3851    CGCCGACCCC GCACCCGCCC CCGAGGCCCA CCGACTCTAG ACTCGAGATC
        GCGGCTGGGG CGTGGGCGGG GGCTCCGGGT GGCTGAGATC TGAGCTCTAG
```

FIG. 9-5

pIRESpuro2W/hepEK_k

```
3901  GATAATCAAC CTCTGGATTA CAAAATTTGT GAAAGATTGA CTGGTATTCT
      CTATTAGTTG GAGACCTAAT GTTTTAAACA CTTTCTAACT GACCATAAGA
3951  TAACTATGTT GCTCCTTTTA CGCTATGTGG ATACGCTGCT TTAATGCCTT
      ATTGATACAA CGAGGAAAAT GCGATACACC TATGCGACGA AATTACGGAA
4001  TGTATCATGC TATTGCTTCC CGTATGGCTT TCATTTTCTC CTCCTTGTAT
      ACATAGTACG ATAACGAAGG GCATACCGAA AGTAAAAGAG GAGGAACATA
4051  AAATCCTGGT TGCTGTCTCT TTATGAGGAG TTGTGGCCCG TTGTCAGGCA
      TTTAGGACCA ACGACAGAGA AATACTCCTC AACACCGGGC AACAGTCCGT
4101  ACGTGGCGTG GTGTGCACTG TGTTTGCTGA CGCAACCCCC ACTGGTTGGG
      TGCACCGCAC CACACGTGAC ACAAACGACT GCGTTGGGGG TGACCAACCC
4151  GCATTGCCAC CACCTGTCAG CTCCTTTCCG GGACTTTCGC TTTCCCCCTC
      CGTAACGGTG GTGGACAGTC GAGGAAAGGC CCTGAAAGCG AAAGGGGGAG
4201  CCTATTGCCA CGGCGGAACT CATCGCCGCC TGCCTTGCCC GCTGCTGGAC
      GGATAACGGT GCCGCCTTGA GTAGCGGCGG ACGGAACGGG CGACGACCTG
4251  AGGGGCTCGG CTGTTGGGCA CTGACAATTC CGTGGTGTTG TCGGGGAAAT
      TCCCCGAGCC GACAACCCGT GACTGTTAAG GCACCACAAC AGCCCCTTTA
4301  CATCGTCCTT TCCTTGGCTG CTCGCCTGTG TTGCCACCTG GATTCTGCGC
      GTAGCAGGAA AGGAACCGAC GAGCGGACAC AACGGTGGAC CTAAGACGCG
4351  GGGACGTCCT TCTGCTACGT CCCTTCGGCC CTCAATCCAG CGGACCTTCC
      CCCTGCAGGA AGACGATGCA GGGAAGCCGG GAGTTAGGTC GCCTGGAAGG
4401  TTCCCGCGGC CTGCTGCCGG CTCTGCGGCC TCTTCCGCGT CTTCGCCTTC
      AAGGGCGCCG GACGACGGCC GAGACGCCGG AGAAGGCGCA GAAGCGGAAG
4451  GCCCTCAGAC GAGTCGGATC TCCCTTTGGG CCGCCTCCCC GCCTGATCGA
      CGGGAGTCTG CTCAGCCTAG AGGGAAACCC GGCGGAGGGG CGGACTAGCT
4501  TCTAGAGCTC GCTGATCAGC CTCGACTGTG CCTTCTAGTT GCCAGCCATC
      AGATCTCGAG CGACTAGTCG GAGCTGACAC GGAAGATCAA CGGTCGGTAG
4551  TGTTGTTTGC CCCTCCCCCG TGCCTTCCTT GACCCTGGAA GGTGCCACTC
      ACAACAAACG GGGAGGGGGC ACGGAAGGAA CTGGGACCTT CCACGGTGAG
4601  CCACTGTCCT TTCCTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT
      GGTGACAGGA AAGGATTATT TTACTCCTTT AACGTAGCGT AACAGACTCA
4651  AGGTGTCATT CTATTCTGGG GGGTGGGGTG GGGCAGGACA GCAAGGGGGA
      TCCACAGTAA GATAAGACCC CCCACCCCAC CCCGTCCTGT CGTTCCCCCT
4701  GGATTGGGAA GACAATAGCA GGCATGCTGG GGATGCGGTG GGCTCTATGG
      CCTAACCCTT CTGTTATCGT CCGTACGACC CCTACGCCAC CCGAGATACC
4751  CTTCTGAGGC GGAAAGAACC AGCTGGGGCT CGAGTGCATT CTAGTTGTGG
      GAAGACTCCG CCTTTCTTGG TCGACCCCGA GCTCACGTAA GATCAACACC
4801  TTTGTCCAAA CTCATCAATG TATCTTATCA TGTCTGTATA CCGTCGACCT
      AAACAGGTTT GAGTAGTTAC ATAGAATAGT ACAGACATAT GGCAGCTGGA
4851  CTAGCTAGAG CTTGGCGTAA TCATGGTCAT AGCTGTTTCC TGTGTGAAAT
      GATCGATCTC GAACCGCATT AGTACCAGTA TCGACAAAGG ACACACTTTA
4901  TGTTATCCGC TCACAATTCC ACACAACATA CGAGCCGGAA GCATAAAGTG
      ACAATAGGCG AGTGTTAAGG TGTGTTGTAT GCTCGGCCTT CGTATTTCAC
4951  TAAAGCCTGG GGTGCCTAAT GAGTGAGCTA ACTCACATTA ATTGCGTTGC
      ATTTCGGACC CCACGGATTA CTCACTCGAT TGAGTGTAAT TAACGCAACG
5001  GCTCACTGCC CGCTTTCCAG TCGGGAAACC TGTCGTGCCA GCTGCATTAA
      CGAGTGACGG GCGAAAGGTC AGCCCTTTGG ACAGCACGGT CGACGTAATT
```

FIG. 9-6

pIRESpuro2W/hepEK_k

```
5051  TGAATCGGCC AACGCGCGGG GAGAGGCGGT TTGCGTATTG GGCGCTCTTC
      ACTTAGCCGG TTGCGCGCCC CTCTCCGCCA AACGCATAAC CCGCGAGAAG
5101  CGCTTCCTCG CTCACTGACT CGCTGCGCTC GGTCGTTCGG CTGCGGCGAG
      GCGAAGGAGC GAGTGACTGA GCGACGCGAG CCAGCAAGCC GACGCCGCTC
5151  CGGTATCAGC TCACTCAAAG GCGGTAATAC GGTTATCCAC AGAATCAGGG
      GCCATAGTCG AGTGAGTTTC CGCCATTATG CCAATAGGTG TCTTAGTCCC
5201  GATAACGCAG GAAAGAACAT GTGAGCAAAA GGCCAGCAAA AGGCCAGGAA
      CTATTGCGTC CTTTCTTGTA CACTCGTTTT CCGGTCGTTT TCCGGTCCTT
5251  CCGTAAAAAG GCCGCGTTGC TGGCGTTTTT CCATAGGCTC CGCCCCCCTG
      GGCATTTTTC CGGCGCAACG ACCGCAAAAA GGTATCCGAG GCGGGGGGAC
5301  ACGAGCATCA CAAAAATCGA CGCTCAAGTC AGAGGTGGCG AAACCCGACA
      TGCTCGTAGT GTTTTTAGCT GCGAGTTCAG TCTCCACCGC TTTGGGCTGT
5351  GGACTATAAA GATACCAGGC GTTTCCCCCT GGAAGCTCCC TCGTGCGCTC
      CCTGATATTT CTATGGTCCG CAAAGGGGGA CCTTCGAGGG AGCACGCGAG
5401  TCCTGTTCCG ACCCTGCCGC TTACCGGATA CCTGTCCGCC TTTCTCCCTT
      AGGACAAGGC TGGGACGGCG AATGGCCTAT GGACAGGCGG AAAGAGGGAA
5451  CGGGAAGCGT GGCGCTTTCT CAATGCTCAC GCTGTAGGTA TCTCAGTTCG
      GCCCTTCGCA CCGCGAAAGA GTTACGAGTG CGACATCCAT AGAGTCAAGC
5501  GTGTAGGTCG TTCGCTCCAA GCTGGGCTGT GTGCACGAAC CCCCCGTTCA
      CACATCCAGC AAGCGAGGTT CGACCCGACA CACGTGCTTG GGGGGCAAGT
5551  GCCCGACCGC TGCGCCTTAT CCGGTAACTA TCGTCTTGAG TCCAACCCGG
      CGGGCTGGCG ACGCGGAATA GGCCATTGAT AGCAGAACTC AGGTTGGGCC
5601  TAAGACACGA CTTATCGCCA CTGGCAGCAG CCACTGGTAA CAGGATTAGC
      ATTCTGTGCT GAATAGCGGT GACCGTCGTC GGTGACCATT GTCCTAATCG
5651  AGAGCGAGGT ATGTAGGCGG TGCTACAGAG TTCTTGAAGT GGTGGCCTAA
      TCTCGCTCCA TACATCCGCC ACGATGTCTC AAGAACTTCA CCACCGGATT
5701  CTACGGCTAC ACTAGAAGGA CAGTATTTGG TATCTGCGCT CTGCTGAAGC
      GATGCCGATG TGATCTTCCT GTCATAAACC ATAGACGCGA GACGACTTCG
5751  CAGTTACCTT CGGAAAAAGA GTTGGTAGCT CTTGATCCGG CAAACAAACC
      GTCAATGGAA GCCTTTTTCT CAACCATCGA GAACTAGGCC GTTTGTTTGG
5801  ACCGCTGGTA GCGGTGGTTT TTTTGTTTGC AAGCAGCAGA TTACGCGCAG
      TGGCGACCAT CGCCACCAAA AAAACAAACG TTCGTCGTCT AATGCGCGTC
5851  AAAAAAAGGA TCTCAAGAAG ATCCTTTGAT CTTTTCTACG GGGTCTGACG
      TTTTTTTCCT AGAGTTCTTC TAGGAAACTA GAAAAGATGC CCCAGACTGC
5901  CTCAGTGGAA CGAAAACTCA CGTTAAGGGA TTTTGGTCAT GAGATTATCA
      GAGTCACCTT GCTTTTGAGT GCAATTCCCT AAAACCAGTA CTCTAATAGT
5951  AAAAGGATCT TCACCTAGAT CCTTTTAAAT TAAAAATGAA GTTTTAAATC
      TTTTCCTAGA AGTGGATCTA GGAAAATTTA ATTTTTACTT CAAAATTTAG
6001  AATCTAAAGT ATATATGAGT AAACTTGGTC TGACAGTTAC CAATGCTTAA
      TTAGATTTCA TATATACTCA TTTGAACCAG ACTGTCAATG GTTACGAATT
6051  TCAGTGAGGC ACCTATCTCA GCGATCTGTC TATTTCGTTC ATCCATAGTT
      AGTCACTCCG TGGATAGAGT CGCTAGACAG ATAAAGCAAG TAGGTATCAA
6101  GCCTGACTCC CCGTCGTGTA GATAACTACG ATACGGGAGG GCTTACCATC
      CGGACTGAGG GGCAGCACAT CTATTGATGC TATGCCCTCC CGAATGGTAG
6151  TGGCCCCAGT GCTGCAATGA TACCGCGAGA CCCACGCTCA CCGGCTCCAG
      ACCGGGGTCA CGACGTTACT ATGGCGCTCT GGGTGCGAGT GGCCGAGGTC
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FIG. 9-7

pIRESpuro2W/hepEK_k

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6201   ATTTATCAGC AATAAACCAG CCAGCCGGAA GGGCCGAGCG CAGAAGTGGT
       TAAATAGTCG TTATTTGGTC GGTCGGCCTT CCCGGCTCGC GTCTTCACCA
6251   CCTGCAACTT TATCCGCCTC CATCCAGTCT ATTAATTGTT GCCGGGAAGC
       GGACGTTGAA ATAGGCGGAG GTAGGTCAGA TAATTAACAA CGGCCCTTCG
6301   TAGAGTAAGT AGTTCGCCAG TTAATAGTTT GCGCAACGTT GTTGCCATTG
       ATCTCATTCA TCAAGCGGTC AATTATCAAA CGCGTTGCAA CAACGGTAAC
6351   CTACAGGCAT CGTGGTGTCA CGCTCGTCGT TTGGTATGGC TTCATTCAGC
       GATGTCCGTA GCACCACAGT GCGAGCAGCA AACCATACCG AAGTAAGTCG
6401   TCCGGTTCCC AACGATCAAG GCGAGTTACA TGATCCCCCA TGTTGTGCAA
       AGGCCAAGGG TTGCTAGTTC CGCTCAATGT ACTAGGGGGT ACAACACGTT
6451   AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT CGTTGTCAGA AGTAAGTTGG
       TTTTCGCCAA TCGAGGAAGC CAGGAGGCTA GCAACAGTCT TCATTCAACC
6501   CCGCAGTGTT ATCACTCATG GTTATGGCAG CACTGCATAA TTCTCTTACT
       GGCGTCACAA TAGTGAGTAC CAATACCGTC GTGACGTATT AAGAGAATGA
6551   GTCATGCCAT CCGTAAGATG CTTTTCTGTG ACTGGTGAGT ACTCAACCAA
       CAGTACGGTA GGCATTCTAC GAAAAGACAC TGACCACTCA TGAGTTGGTT
6601   GTCATTCTGA GAATAGTGTA TGCGGCGACC GAGTTGCTCT TGCCCGGCGT
       CAGTAAGACT CTTATCACAT ACGCCGCTGG CTCAACGAGA ACGGGCCGCA
6651   CAATACGGGA TAATACCGCG CCACATAGCA GAACTTTAAA AGTGCTCATC
       GTTATGCCCT ATTATGGCGC GGTGTATCGT CTTGAAATTT TCACGAGTAG
6701   ATTGGAAAAC GTTCTTCGGG GCGAAAACTC TCAAGGATCT TACCGCTGTT
       TAACCTTTTG CAAGAAGCCC CGCTTTTGAG AGTTCCTAGA ATGGCGACAA
6751   GAGATCCAGT TCGATGTAAC CCACTCGTGC ACCCAACTGA TCTTCAGCAT
       CTCTAGGTCA AGCTACATTG GGTGAGCACG TGGGTTGACT AGAAGTCGTA
6801   CTTTTACTTT CACCAGCGTT TCTGGGTGAG CAAAAACAGG AAGGCAAAAT
       GAAAATGAAA GTGGTCGCAA AGACCCACTC GTTTTTGTCC TTCCGTTTTA
6851   GCCGCAAAAA AGGGAATAAG GGCGACACGG AAATGTTGAA TACTCATACT
       CGGCGTTTTT TCCCTTATTC CCGCTGTGCC TTTACAACTT ATGAGTATGA
6901   CTTCCTTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT TGTCTCATGA
       GAAGGAAAAA GTTATAATAA CTTCGTAAAT AGTCCCAATA ACAGAGTACT
6951   GCGGATACAT ATTTGAATGT ATTTAGAAAA ATAAACAAAT AGGGGTTCCG
       CGCCTATGTA TAAACTTACA TAAATCTTTT TATTTGTTTA TCCCCAAGGC
7001   CGCACATTTC CCCGAAAAGT GCCACCTGAC GTC
       GCGTGTAAAG GGGCTTTTCA CGGTGGACTG CAG
```

FIG. 10-1

pCEP4W/hepEK

```
  1 . TCGAGCGGCC GCTTTAAACT CAATGGTGAT GGTGATGATG ACCGGTACGC
       AGCTCGCCGG CGAAATTTGA GTTACCACTA CCACTACTAC TGGCCATGCG
 -3                          H   H   H   H   H   H   G   T·R  T
 51    GTAGAATCGA GACCGAGGAG AGGGTTAGGG ATAGGCTTAC CGAATTCGAG
       CATCTTAGCT CTGGCTCCTC TCCCAATCCC TATCCGAATG GCTTAAGCTC
 -3    ·T  S  D  L  G  L  L  P  N  P  I  P  K  G  F  E  L
101    CTGGGTCACC ATGCCGCTGG CTTCGGAGTG AGTCTTTATG GCCTGGAAGA
       GACCCAGTGG TACGGCGACC GAAGCCTCAC TCAGAAATAC CGGACCTTCT
 -3    Q  T  V  M  G  S  A  E  S ·H  T  K  I  A  Q  F  I·
151    TCCACTCCCG GAAGTCACTG ACTTTGGTGT AGACGCCTGG CTTCTGGGCC
       AGGTGAGGGC CTTCAGTGAC TGAAACCACA TCTGCGGACC GAAGACCCGG
 -3    ·I  W  E  R  F  D  S  V  K  T  Y  V  G  P  K  Q  A  L
201    AGGGCACAGC CAGTGCCCCA ACTCACAATG CCACACAGCC GCCAACGTGG
       TCCCGTGTCG GTCACGGGGT TGAGTGTTAC GGTGTGTCGG CGGTTGCACC
 -3    ·L  A  C  G  T  G  W  S  V  I  G  C  L  R  W  R  P
251    CGTCCGAGAG ATGCTGTCCT CACACACAAA GGGACCACCG CTGTCGCCCT
       GCAGGCTCTC TACGACAGGA GTGTGTGTTT CCCTGGTGGC GACAGCGGGA
 -3    T  R  S  I  S  D  E  C  V  F  P  G  G  S  D  G  Q·
301    GGCAGGCATC AATGCCACCC TCGGGGTAGC CAGCACAGAA CATCTTGGGC
       CCGTCCGTAG TTACGGTGGG AGCCCCATCG GTCGTGTCTT GTAGAACCCG
 -3    ·Q  C  A  D  I  G  G  E  P  Y  G  A  C  F  M  K  P  K
351    TTGATCTGGT TTCCATAGAA ATCAGCGCCA TTGCAGACAT CATTGCTGAT
       AACTAGACCA AAGGTATCTT TAGTCGCGGT AACGTCTGTA GTAACGACTA
 -3    ·K  I  Q  N  G  Y  F  D  A  G  N  C  V  D  N  S  I
401    TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT
       ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA
 -3    I  P  V  R  A  E  Q  L  V  G  A  Q  Q  G  Y  Y  Q·
451    GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC
       CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG
 -3    ·Q  T  N  G  W  G  T  V  T  C  I  K  G  D  V  L  A  Q
501    TGGCCGGCAG CTGGGAGGCA CACAGGCTGG ATGTATTCTG TGAGGGGCAG
       ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCCGTC
 -3    ·Q  G  A  A  P  L  C  V  P  Q  I  Y  E  T  L  P  L
551    GGGACTGGAG AGGTGGACCA GGGCAATATC GTTGCTGTTC TCCTCGCTGT
       CCCTGACCTC TCCACCTGGT CCCGTTATAG CAACGACAAG AGGAGCGACA
 -3  · P  S  S  L  H  V  L  A  I  D  N  S  N  E  E  S  N·
601    TGGGGTCCCG AAAGGGAAGA TAGCCCCCGT GGTAGACCAC AGCCTGCACC
       ACCCCAGGGC TTTCCCTTCT ATCGGGGGCA CCATCTGGTG TCGGACGTGG
 -3    ·N  P  D  R  F  P  L  Y  G  G  H  Y  V  V  A  Q  V  G
651    CCCAGCTGCA GACCGTGGGG AGAGGCCTGG CCACGGCAC CGGCAAACAC
       GGGTCGACGT CTGGCACCCC TCTCCGGACC CGGTGCCGTG GCCGTTTGTG
 -3    ·G  L  Q  L  G  H  P  S  A ·Q  A  V  A  G  A  F  V
701    TCGCCATCGG GACAGGACCC GGTTCCGCTC CGGGAAGCAG TGGGCGGCTG
       AGCGGTAGCC CTGTCCTGGG CCAAGGCGAG GCCCTTCGTC ACCCGCCGAC
 -3    R  W  R  S  L  V  R  N  R  E  P  F  C  H  A  A  T·
```

FIG. 10-2

pCEP4W/hepEK

```
 751  TCAGCACCCA GTCCCCGGAG AGCAGGGATC CCCCACAGAG GTGTGCTCCA
      AGTCGTGGGT CAGGGGCCTC TCGTCCCTAG GGGGTGTCTC CACACGAGGT
  -3  ·T  L  V  W  D  G  S  L  L  S  G  G  C  L  H  A  G  D
 801  TCATAGCGAA GGCTGACTTG CCACGGCCAC CGGCCCAAGC TGGTGTCCCG
      AGTATCGCTT CCGACTGAAC GGTGCCGGTG GCCGGGTTCG ACCACAGGGC
  -3  ·D  Y  R  L  S  V  Q  W  P  W  R  G  L  S  T  D  R
 851  GCCTCCCACG ATCTTGTCGT CGTCGTCCAC GGGCAGCTTC CTGCGGCCAC
      CGGAGGGTGC TAGAACAGCA GCAGCAGGTG CCCGTCGAAG GACGCCGGTG
  -3   G  G  V  I  K  D  D  D  D  V  P  L  K  R  R  G  C·
 901  AGTCTTGGCA GATGGCGGCC AAGAAACGGC CTCTGGGGCA ATCACACACG
      TCAGAACCGT CTACCGCCGG TTCTTTGCCG GAGACCCCGT TAGTGTGTGC
  -3  ·C  D  Q  C  I  A  A  L  F  R  G  R  P  C  D  C  V  S
 951  GAGATGACCT CCAGCAGCCT CTGGGTGTGG GGCAGCCTCC CCTCGTCCAC
      CTCTACTGGA GGTCGTCGGA GACCCACACC CCGTCGGAGG GGAGCAGGTG
  -3  ·S  I  V  E  L  L  R  Q  T  H  P  L  R  G  E  D  V
1001  ACAGAAGAAG CCCGACGTGC CATTGGCGCC CGCCGTTCGC ACGTCCAGCT
      TGTCTTCTTC GGGCTGCACG GTAACCGCGG GCGGCAAGCG TGCAGGTCGA
  -3   C  F  F  G  S  T  G  N  A  G  A  T  R  V  D  L  E·
1051  CGGAGTGGGT CAGTGCCCTG AGGAAGCCCA TCTCCTCGCA GCTGAGTCCG
      GCCTCACCCA GTCACGGGAC TCCTTCGGGT AGAGGAGCGT CGACTCAGGC
  -3  ·E  S  H  T  L  A  R  L  F  G  M  E  E  C  S  L  G  A·
1101  GCTACCCTGG CGTTAGAGCG CGAGGAGCAC AGCAGCCGCC ACGTCCCTTC
      CGATGGGACC GCAATCTCGC GCTCCTCGTG TCGTCGGCGG TGCAGGGAAG
  -3  ·A  V  R  A  N  S  R  S  S  C  L  L  R  W  T  G  E
1151  CGTCTTGTCA AAGACCATGA GCCGAGCGTC CGCAGAGCTG ACCTGCACTG
      GCAGAACAGT TTCTGGTACT CGGCTCGCAG GCGTCTCGAC TGGACGTGAC
  -3   T  K  D  F  V  M  L  R  A  D  A  S  S  V  Q  V  P·
1201  GGTACAGCGG CTCCTGGTCA CTCCTATCCG GAGCGTCACC AGTGGAACCT
      CCATGTCGCC GAGGACCAGT GAGGATAGGC CTCGCAGTGG TCACCTTGGA
  -3  ·P  Y  L  P  E  Q  D  S  R  D  P  A  D  G  T  S  G  P·
1251  GGAACCCAGA GCAGCAGTAC CCATAGCAGG AGTGTGTCTG TCTCCATGGT
      CCTTGGGTCT CGTCGTCATG GGTATCGTCC TCACACAGAC AGAGGTACCA
  -3  ·P  V  W  L  L  L  V  W  L  L  L  T  D  T  E  M
1301  GGCGATCTGG TACCCAGCTT CTAGAGATCT GACGGTTCAC TAAACGAGCT
      CCGCTAGACC ATGGGTCGAA GATCTCTAGA CTGCCAAGTG ATTTGCTCGA
1351  CTGCTTATAT AGACCTCCCA CCGTACACGC CTACCGCCCA TTTGCGTCAA
      GACGAATATA TCTGGAGGGT GGCATGTGCG GATGGCGGGT AAACGCAGTT
1401  CGGGGCGGGG TTATTACGAC ATTTTGGAAA GTCCCGTTGA TTTTGGTGCC
      GCCCCGCCCC AATAATGCTG TAAAACCTTT CAGGGCAACT AAAACCACGG
1451  AAAACAAACT CCCATTGACG TCAATGGGGT GGAGACTTGG AAATCCCCGT
      TTTTGTTTGA GGGTAACTGC AGTTACCCCA CCTCTGAACC TTTAGGGGCA
1501  GAGTCAAACC GCTATCCACG CCCATTGGTG TACTGCCAAA ACCGCATCAC
      CTCAGTTTGG CGATAGGTGC GGGTAACCAC ATGACGGTTT TGGCGTAGTG
1551  CATGGTAATA GCGATGACTA ATACGTAGAT GTACTGCCAA GTAGGAAAGT
      GTACCATTAT CGCTACTGAT TATGCATCTA CATGACGGTT CATCCTTTCA
```

FIG. 10-3

pCEP4W/hepEK

```
1601   CCCGTAAGGT  CATGTACTGG  GCATAATGCC  AGGCGGGCCA  TTTACCGTCA
       GGGCATTCCA  GTACATGACC  CGTATTACGG  TCCGCCCGGT  AAATGGCAGT
1651   TTGACGTCAA  TAGGGGGCGG  ACTTGGCATA  TGATACACTT  GATGTACTGC
       AACTGCAGTT  ATCCCCCGCC  TGAACCGTAT  ACTATGTGAA  CTACATGACG
1701   CAAGTGGGCA  GTTTACCGTA  AATACTCCAC  CCATTGACGT  CAATGGAAAG
       GTTCACCCGT  CAAATGGCAT  TTATGAGGTG  GGTAACTGCA  GTTACCTTTC
1751   TCCCTATTGG  CGTTACTATG  GGAACATACG  TCATTATTGA  CGTCAATGGG
       AGGGATAACC  GCAATGATAC  CCTTGTATGC  AGTAATAACT  GCAGTTACCC
1801   CGGGGGTCGT  TGGGCGGTCA  GCCAGGCGGG  CCATTTACCG  TAAGTTATGT
       GCCCCCAGCA  ACCCGCCAGT  CGGTCCGCCC  GGTAAATGGC  ATTCAATACA
1851   AACGCGGAAC  TCCATATATG  GGCTATGAAC  TAATGACCCC  GTAATTGATT
       TTGCGCCTTG  AGGTATATAC  CCGATACTTG  ATTACTGGGG  CATTAACTAA
1901   ACTATTAATA  ACTAGTCAAT  AATCAATGTC  AACATGGCGG  TCATATTGGA
       TGATAATTAT  TGATCAGTTA  TTAGTTACAG  TTGTACCGCC  AGTATAACCT
1951   CATGAGCCAA  TATAAATGTA  CATATTATGA  TATAGATACA  ACGTATGCAA
       GTACTCGGTT  ATATTTACAT  GTATAATACT  ATATCTATGT  TGCATACGTT
2001   TGGCCAATAG  CCAATATTGA  TTTATGCTAT  ATAACCAATG  ACTAATATGG
       ACCGGTTATC  GGTTATAACT  AAATACGATA  TATTGGTTAC  TGATTATACC
2051   CTAATTGCCA  ATATTGATTC  AATGTATAGA  TCTTCCATAC  CTACCAGTTC
       GATTAACGGT  TATAACTAAG  TTACATATCT  AGAAGGTATG  GATGGTCAAG
2101   TGCGCCTGCA  GCAATGCAAC  AACGTTGCCC  GGATCTGCGA  TGATAAGCTG
       ACGCGGACGT  CGTTACGTTG  TTGCAACGGG  CCTAGACGCT  ACTATTCGAC
2151   TCAAACATGA  GAATTGGTCG  ACTAGCTTGG  CACGCCAGAA  ATCCGCGCGG
       AGTTTGTACT  CTTAACCAGC  TGATCGAACC  GTGCGGTCTT  TAGGCGCGCC
2201   TGGTTTTTGG  GGGTCGGGGG  TGTTTGGCAG  CCACAGACGC  CCGGTGTTCG
       ACCAAAAACC  CCCAGCCCCC  ACAAACCGTC  GGTGTCTGCG  GGCCACAAGC
2251   TGTCGCGCCA  GTACATGCGG  TCCATGCCCA  GGCCATCCAA  AAACCATGGG
       ACAGCGCGGT  CATGTACGCC  AGGTACGGGT  CCGGTAGGTT  TTTGGTACCC
2301   TCTGTCTGCT  CAGTCCAGTC  GTGGACCAGA  CCCCACGCAA  CGCCCAAAAT
       AGACAGACGA  GTCAGGTCAG  CACCTGGTCT  GGGGTGCGTT  GCGGGTTTTA
2351   AATAACCCCC  ACGAACCATA  AACCATTCCC  CATGGGGGAC  CCCGTCCCTA
       TTATTGGGGG  TGCTTGGTAT  TTGGTAAGGG  GTACCCCCTG  GGGCAGGGAT
2401   ACCCACGGGG  CCAGTGGCTA  TGGCAGGGCC  TGCCGCCCCG  ACGTTGGCTG
       TGGGTGCCCC  GGTCACCGAT  ACCGTCCCGG  ACGGCGGGGC  TGCAACCGAC
2451   CGAGCCCTGG  GCCTTCACCC  GAACTTGGGG  GGTGGGGTGG  GGAAAAGGAA
       GCTCGGGACC  CGGAAGTGGG  CTTGAACCCC  CCACCCCACC  CCTTTTCCTT
2501   GAAACGCGGG  CGTATTGGCC  CCAATGGGGT  CTCGGTGGGG  TATCGACAGA
       CTTTGCGCCC  GCATAACCGG  GGTTACCCCA  GAGCCACCCC  ATAGCTGTCT
2551   GTGCCAGCCC  TGGGACCGAA  CCCCGCGTTT  ATGAACAAAC  GACCCAACAC
       CACGGTCGGG  ACCCTGGCTT  GGGGCGCAAA  TACTTGTTTG  CTGGGTTGTG
2601   CCGTGCGTTT  TATTCTGTCT  TTTTATTGCC  GTCATAGCGC  GGGTTCCTTC
       GGCACGCAAA  ATAAGACAGA  AAAATAACGG  CAGTATCGCG  CCCAAGGAAG
2651   CGGTATTGTC  TCCTTCCGTG  TTTCAGTTAG  CCTCCCCCAT  CTCCCCTATT
       GCCATAACAG  AGGAAGGCAC  AAAGTCAATC  GGAGGGGGTA  GAGGGGATAA
2701   CCTTTGCCCT  CGGACGAGTG  CTGGGGCGTC  GGTTCCACT   ATCGGCGAGT
       GGAAACGGGA  GCCTGCTCAC  GACCCCGCAG  CCAAAGGTGA  TAGCCGCTCA
```

FIG. 10-4

pCEP4W/hepEK

```
2751  ACTTCTACAC AGCCATCGGT CCAGACGGCC GCGCTTCTGC GGGCGATTTG
      TGAAGATGTG TCGGTAGCCA GGTCTGCCGG CGCGAAGACG CCCGCTAAAC
2801  TGTACGCCCG ACAGTCCCGG CTCCGGATCG GACGATTGCG TCGCATCGAC
      ACATGCGGGC TGTCAGGGCC GAGGCCTAGC CTGCTAACGC AGCGTAGCTG
2851  CCTGCGCCCA AGCTGCATCA TCGAAATTGC CGTCAACCAA GCTCTGATAG
      GGACGCGGGT TCGACGTAGT AGCTTTAACG GCAGTTGGTT CGAGACTATC
2901  AGTTGGTCAA GACCAATGCG GAGCATATAC GCCCGGAGCC GCGGCGATCC
      TCAACCAGTT CTGGTTACGC CTCGTATATG CGGGCCTCGG CGCCGCTAGG
2951  TGCAAGCTCC GGATGCCTCC GCTCGAAGTA GCGCGTCTGC TGCTCCATAC
      ACGTTCGAGG CCTACGGAGG CGAGCTTCAT CGCGCAGACG ACGAGGTATG
3001  AAGCCAACCA CGGCCTCCAG AAGAAGATGT TGGCGACCTC GTATTGGGAA
      TTCGGTTGGT GCCGGAGGTC TTCTTCTACA ACCGCTGGAG CATAACCCTT
3051  TCCCCGAACA TCGCCTCGCT CCAGTCAATG ACCGCTGTTA TGCGGCCATT
      AGGGGCTTGT AGCGGAGCGA GGTCAGTTAC TGGCGACAAT ACGCCGGTAA
3101  GTCCGTCAGG ACATTGTTGG AGCCGAAATC CGCGTGCACG AGGTGCCGGA
      CAGGCAGTCC TGTAACAACC TCGGCTTTAG GCGCACGTGC TCCACGGCCT
3151  CTTCGGGGCA GTCCTCGGCC CAAAGCATCA GCTCATCGAG AGCCTGCGCG
      GAAGCCCCGT CAGGAGCCGG GTTTCGTAGT CGAGTAGCTC TCGGACGCGC
3201  ACGGACGCAC TGACGGTGTC GTCCATCACA GTTTGCCAGT GATACACATG
      TGCCTGCGTG ACTGCCACAG CAGGTAGTGT CAAACGGTCA CTATGTGTAC
3251  GGGATCAGCA ATCGCGCATA TGAAATCACG CCATGTAGTG TATTGACCGA
      CCCTAGTCGT TAGCGCGTAT ACTTTAGTGC GGTACATCAC ATAACTGGCT
3301  TTCCTTGCGG TCCGAATGGG CCGAACCCGC TCGTCTGGCT AAGATCGGCC
      AAGGAACGCC AGGCTTACCC GGCTTGGGCG AGCAGACCGA TTCTAGCCGG
3351  GCAGCGATCG CATCCATGGC CTCCGCGACC GGCTGCAGAA CAGCGGGCAG
      CGTCGCTAGC GTAGGTACCG GAGGCGCTGG CCGACGTCTT GTCGCCCGTC
3401  TTCGGTTTCA GGCAGGTCTT GCAACGTGAC ACCCTGTGCA CGGCGGGAGA
      AAGCCAAAGT CCGTCCAGAA CGTTGCACTG TGGGACACGT GCCGCCCTCT
3451  TGCAATAGGT CAGGCTCTCG CTGAATTCCC CAATGTCAAG CACTTCCGGA
      ACGTTATCCA GTCCGAGAGC GACTTAAGGG GTTACAGTTC GTGAAGGCCT
3501  ATCGGGAGCG CGGCCGATGC AAAGTGCCGA TAAACATAAC GATCTTTGTA
      TAGCCCTCGC GCCGGCTACG TTTCACGGCT ATTTGTATTG CTAGAAACAT
3551  GAAACCATCG GCGCAGCTAT TTACCCGCAG GACATATCCA CGCCCTCCTA
      CTTTGGTAGC CGCGTCGATA AATGGGCGTC CTGTATAGGT GCGGGAGGAT
3601  CATCGAAGCT GAAAGCACGA GATTCTTCGC CCTCCGAGAG CTGCATCAGG
      GTAGCTTCGA CTTTCGTGCT CTAAGAAGCG GGAGGCTCTC GACGTAGTCC
3651  TCGGAGACGC TGTCGAACTT TTCGATCAGA AACTTCTCGA CAGACGTCGC
      AGCCTCTGCG ACAGCTTGAA AAGCTAGTCT TTGAAGAGCT GTCTGCAGCG
3701  GGTGAGTTCA GGCTTTTTCA TATCTCATTG CCCGGGATCT GCGGCACGCT
      CCACTCAAGT CCGAAAAAGT ATAGAGTAAC GGGCCCTAGA CGCCGTGCGA
3751  GTTGACGCTG TTAAGCGGGT CGCTGCAGGG TCGCTCGGTG TTCGAGGCCA
      CAACTGCGAC AATTCGCCCA GCGACGTCCC AGCGAGCCAC AAGCTCCGGT
3801  CACGCGTCAC CTTAATATGC GAAGTGGACC TGGGACCGCG CCGCCCCGAC
      GTGCGCAGTG GAATTATACG CTTCACCTGG ACCCTGGCGC GGCGGGGCTG
3851  TGCATCTGCG TGTTCGAATT CGCCAATGAC AAGACGCTGG GCGGGGTTTG
      ACGTAGACGC ACAAGCTTAA GCGGTTACTG TTCTGCGACC CGCCCCAAAC
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FIG. 10-5

pCEP4W/hepEK

```
3901   TGTCATCATA GAACTAAAGA CATGCAAATA TATTTCTTCC GGGGACACCG
       ACAGTAGTAT CTTGATTTCT GTACGTTTAT ATAAAGAAGG CCCCTGTGGC
3951   CCAGCAAACG CGAGCAACGG GCCACGGGGA TGAAGCAGGG CATGGCGGCC
       GGTCGTTTGC GCTCGTTGCC CGGTGCCCCT ACTTCGTCCC GTACCGCCGG
4001   GACGCGCTGG GCTACGTCTT GCTGGCGTTC GCGACGCGAG GCTGGATGGC
       CTGCGCGACC CGATGCAGAA CGACCGCAAG CGCTGCGCTC CGACCTACCG
4051   CTTCCCCATT ATGATTCTTC TCGCTTCCGG CGGCATCGGG ATGCCCGCGT
       GAAGGGGTAA TACTAAGAAG AGCGAAGGCC GCCGTAGCCC TACGGGCGCA
4101   TGCAGGCCAT GCTGTCCAGG CAGGTAGATG ACGACCATCA GGACAGCTT
       ACGTCCGGTA CGACAGGTCC GTCCATCTAC TGCTGGTAGT CCCTGTCGAA
4151   CAAGGATCGC TCGCGGCTCT TACCAGCCTA ACTTCGATCA CTGGACCGCT
       GTTCCTAGCG AGCGCCGAGA ATGGTCGGAT TGAAGCTAGT GACCTGGCGA
4201   GATCGTCACG GCGATTTATG CCGCCTCGGC GAGCACATGG AACGGGTTGG
       CTAGCAGTGC CGCTAAATAC GGCGGAGCCG CTCGTGTACC TTGCCCAACC
4251   CATGGATTGT AGGCGCCGCC CTATACCTTG TCTGCCTCCC CGCGTTGCGT
       GTACCTAACA TCCGCGGCGG GATATGGAAC AGACGGAGGG GCGCAACGCA
4301   CGCGGTGCAT GGAGCCGGGC CACCTCGACC TGAATGGAAG CCGGCGGCAC
       GCGCCACGTA CCTCGGCCCG GTGGAGCTGG ACTTACCTTC GGCCGCCGTG
4351   CTCGCTAACG GATTCACCAC TCCAAGAATT GGAGCCAATC AATTCTTGCG
       GAGCGATTGC CTAAGTGGTG AGGTTCTTAA CCTCGGTTAG TTAAGAACGC
4401   GAGAACTGTG AATGCGCAAA CCAACCCTTG GCAGAACATA TCCATCGCGT
       CTCTTGACAC TTACGCGTTT GGTTGGGAAC CGTCTTGTAT AGGTAGCGCA
4451   CCGCCATCTC CAGCAGCCGC ACGCGGCGCA GCAAAAGGCC AGGAACCGTA
       GGCGGTAGAG GTCGTCGGCG TGCGCCGCGT CGTTTTCCGG TCCTTGGCAT
4501   AAAAGGCCGC GTTGCTGGCG TTTTTCCATA GGCTCCGCCC CCCTGACGAG
       TTTTCCGGCG CAACGACCGC AAAAAGGTAT CCGAGGCGGG GGGACTGCTC
4551   CATCACAAAA ATCGACGCTC AAGTCAGAGG TGGCGAAACC CGACAGGACT
       GTAGTGTTTT TAGCTGCGAG TTCAGTCTCC ACCGCTTTGG GCTGTCCTGA
4601   ATAAAGATAC CAGGCGTTTC CCCCTGGAAG CTCCCTCGTG CGCTCTCCTG
       TATTTCTATG GTCCGCAAAG GGGGACCTTC GAGGGAGCAC GCGAGAGGAC
4651   TTCCGACCCT GCCGCTTACC GGATACCTGT CCGCCTTTCT CCCTTCGGGA
       AAGGCTGGGA CGGCGAATGG CCTATGGACA GGCGGAAAGA GGGAAGCCCT
4701   AGCGTGGCGC TTTCTCATAG CTCACGCTGT AGGTATCTCA GTTCGGTGTA
       TCGCACCGCG AAAGAGTATC GAGTGCGACA TCCATAGAGT CAAGCCACAT
4751   GGTCGTTCGC TCCAAGCTGG GCTGTGTGCA CGAACCCCCC GTTCAGCCCG
       CCAGCAAGCG AGGTTCGACC CGACACACGT GCTTGGGGGG CAAGTCGGGC
4801   ACCGCTGCGC CTTATCCGGT AACTATCGTC TTGAGTCCAA CCCGGTAAGA
       TGGCGACGCG GAATAGGCCA TTGATAGCAG AACTCAGGTT GGGCCATTCT
4851   CACGACTTAT CGCCACTGGC AGCAGCCACT GGTAACAGGA TTAGCAGAGC
       GTGCTGAATA GCGGTGACCG TCGTCGGTGA CCATTGTCCT AATCGTCTCG
4901   GAGGTATGTA GGCGGTGCTA CAGAGTTCTT GAAGTGGTGG CCTAACTACG
       CTCCATACAT CCGCCACGAT GTCTCAAGAA CTTCACCACC GGATTGATGC
4951   GCTACACTAG AAGGACAGTA TTTGGTATCT GCGCTCTGCT GAAGCCAGTT
       CGATGTGATC TTCCTGTCAT AAACCATAGA CGCGAGACGA CTTCGGTCAA
5001   ACCTTCGGAA AAAGAGTTGG TAGCTCTTGA TCCGGCAAAC AAACCACCGC
       TGGAAGCCTT TTTCTCAACC ATCGAGAACT AGGCCGTTTG TTTGGTGGCG
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FIG. 10-6

pCEP4W/hepEK

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5051    TGGTAGCGGT GGTTTTTTTG TTTGCAAGCA GCAGATTACG CGCAGAAAAA
        ACCATCGCCA CCAAAAAAAC AAACGTTCGT CGTCTAATGC GCGTCTTTTT

5101    AAGGATCTCA AGAAGATCCT TTGATCTTTT CTACGGGGTC TGACGCTCAG
        TTCCTAGAGT TCTTCTAGGA AACTAGAAAA GATGCCCCAG ACTGCGAGTC

5151    TGGAACGAAA ACTCACGTTA AGGGATTTTG GTCATGAGAT TATCAAAAAG
        ACCTTGCTTT TGAGTGCAAT TCCCTAAAAC CAGTACTCTA ATAGTTTTTC

5201    GATCTTCACC TAGATCCTTT TAAATTAAAA ATGAAGTTTT AAATCAATCT
        CTAGAAGTGG ATCTAGGAAA ATTTAATTTT TACTTCAAAA TTTAGTTAGA

5251    AAAGTATATA TGAGTAAACT TGGTCTGACA GTTACCAATG CTTAATCAGT
        TTTCATATAT ACTCATTTGA ACCAGACTGT CAATGGTTAC GAATTAGTCA

5301    GAGGCACCTA TCTCAGCGAT CTGTCTATTT CGTTCATCCA TAGTTGCCTG
        CTCCGTGGAT AGAGTCGCTA GACAGATAAA GCAAGTAGGT ATCAACGGAC

5351    ACTCCCCGTC GTGTAGATAA CTACGATACG GGAGGGCTTA CCATCTGGCC
        TGAGGGGCAG CACATCTATT GATGCTATGC CCTCCCGAAT GGTAGACCGG

5401    CCAGTGCTGC AATGATACCG CGAGACCCAC GCTCACCGGC TCCAGATTTA
        GGTCACGACG TTACTATGGC GCTCTGGGTG CGAGTGGCCG AGGTCTAAAT

5451    TCAGCAATAA ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA GTGGTCCTGC
        AGTCGTTATT TGGTCGGTCG GCCTTCCCGG CTCGCGTCTT CACCAGGACG

5501    AACTTTATCC GCCTCCATCC AGTCTATTAA TTGTTGCCGG GAAGCTAGAG
        TTGAAATAGG CGGAGGTAGG TCAGATAATT AACAACGGCC CTTCGATCTC

5551    TAAGTAGTTC GCCAGTTAAT AGTTTGCGCA ACGTTGTTGC CATTGCTGCA
        ATTCATCAAG CGGTCAATTA TCAAACGCGT TGCAACAACG GTAACGACGT

5601    GGCATCGTGG TGTCACGCTC GTCGTTTGGT ATGGCTTCAT TCAGCTCCGG
        CCGTAGCACC ACAGTGCGAG CAGCAAACCA TACCGAAGTA AGTCGAGGCC

5651    TTCCCAACGA TCAAGGCGAG TTACATGATC CCCCATGTTG TGCAAAAAAG
        AAGGGTTGCT AGTTCCGCTC AATGTACTAG GGGGTACAAC ACGTTTTTTC

5701    CGGTTAGCTC CTTCGGTCCT CCGATCGTTG TCAGAAGTAA GTTGGCCGCA
        GCCAATCGAG GAAGCCAGGA GGCTAGCAAC AGTCTTCATT CAACCGGCGT

5751    GTGTTATCAC TCATGGTTAT GGCAGCACTG CATAATTCTC TTACTGTCAT
        CACAATAGTG AGTACCAATA CCGTCGTGAC GTATTAAGAG AATGACAGTA

5801    GCCATCCGTA AGATGCTTTT CTGTGACTGG TGAGTACTCA ACCAAGTCAT
        CGGTAGGCAT TCTACGAAAA GACACTGACC ACTCATGAGT TGGTTCAGTA

5851    TCTGAGAATA GTGTATGCGG CGACCGAGTT GCTCTTGCCC GGCGTCAACA
        AGACTCTTAT CACATACGCC GCTGGCTCAA CGAGAACGGG CCGCAGTTGT

5901    CGGGATAATA CCGCGCCACA TAGCAGAACT TTAAAAGTGC TCATCATTGG
        GCCCTATTAT GGCGCGGTGT ATCGTCTTGA AATTTTCACG AGTAGTAACC

5951    AAAACGTTCT TCGGGGCGAA AACTCTCAAG GATCTTACCG CTGTTGAGAT
        TTTTGCAAGA AGCCCGCTT TTGAGAGTTC CTAGAATGGC GACAACTCTA

6001    CCAGTTCGAT GTAACCCACT CGTGCACCCA ACTGATCTTC AGCATCTTTT
        GGTCAAGCTA CATTGGGTGA GCACGTGGGT TGACTAGAAG TCGTAGAAAA

6051    ACTTTCACCA GCGTTTCTGG GTGAGCAAAA ACAGGAAGGC AAAATGCCGC
        TGAAAGTGGT CGCAAAGACC CACTCGTTTT TGTCCTTCCG TTTTACGGCG

6101    AAAAAAGGGA ATAAGGGCGA CACGGAAATG TTGAATACTC ATACTCTTCC
        TTTTTTCCCT TATTCCCGCT GTGCCTTTAC AACTTATGAG TATGAGAAGG

6151    TTTTTCAATA TTATTGAAGC ATTTATCAGG GTTATTGTCT CATGAGCGGA
        AAAAAGTTAT AATAACTTCG TAAATAGTCC CAATAACAGA GTACTCGCCT
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FIG. 10-7

pCEP4W/hepEK

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6201   TACATATTTG AATGTATTTA GAAAAATAAA CAAATAGGGG TTCCGCGCAC
       ATGTATAAAC TTACATAAAT CTTTTTATTT GTTTATCCCC AAGGCGCGTG
6251   ATTTCCCCGA AAAGTGCCAC CTGACGTCTA AGAAACCATT ATTATCATGA
       TAAAGGGGCT TTTCACGGTG GACTGCAGAT TCTTTGGTAA TAATAGTACT
6301   CATTAACCTA TAAAAATAGG CGTATCACGA GGCCCTTTCG TCTTCAAGAA
       GTAATTGGAT ATTTTTATCC GCATAGTGCT CCGGGAAAGC AGAAGTTCTT
6351   TTCTCATGTT TGACAGCTTA TCATCGATAA GCTGATCCTC ACAGGCCGCA
       AAGAGTACAA ACTGTCGAAT AGTAGCTATT CGACTAGGAG TGTCCGGCGT
6401   CCCAGCTTTT CTTCCGTTGC CCCAGTAGCA TCTCTGTCTG GTGACCTTGA
       GGGTCGAAAA GAAGGCAACG GGGTCATCGT AGAGACAGAC CACTGGAACT
6451   AGAGGAAGAG GAGGGGTCCC GAGAATCCCC ATCCCTACCG TCCAGCAAAA
       TCTCCTTCTC CTCCCCAGGG CTCTTAGGGG TAGGGATGGC AGGTCGTTTT
6501   AGGGGGACGA GGAATTTGAG GCCTGGCTTG AGGCTCAGGA CGCAAATCTT
       TCCCCCTGCT CCTTAAACTC CGGACCGAAC TCCGAGTCCT GCGTTTAGAA
6551   GAGGATGTTC AGCGGGAGTT TTCCGGGCTG CGAGTAATTG GTGATGAGGA
       CTCCTACAAG TCGCCCTCAA AAGGCCCGAC GCTCATTAAC CACTACTCCT
6601   CGAGGATGGT TCGGAGGATG GGGAATTTTC AGACCTGGAT CTGTCTGACA
       GCTCCTACCA AGCCTCCTAC CCCTTAAAAG TCTGGACCTA GACAGACTGT
6651   GCGACCATGA AGGGGATGAG GGTGGGGGGG CTGTTGGAGG GGGCAGGAGT
       CGCTGGTACT TCCCCTACTC CCACCCCCCC GACAACCTCC CCCGTCCTCA
6701   CTGCACTCCC TGTATTCACT GAGCGTCGTC TAATAAAGAT GTCTATTGAT
       GACGTGAGGG ACATAAGTGA CTCGCAGCAG ATTATTTCTA CAGATAACTA
6751   CTCTTTTAGT GTGAATCATG TCTGACGAGG GGCCAGGTAC AGGACCTGGA
       GAGAAAATCA CACTTAGTAC AGACTGCTCC CCGGTCCATG TCCTGGACCT
6801   AATGGCCTAG GAGAGAAGGG AGACACATCT GGACCAGAAG GCTCCGGCGG
       TTACCGGATC CTCTCTTCCC TCTGTGTAGA CCTGGTCTTC CGAGGCCGCC
6851   CAGTGGACCT CAAAGAAGAG GGGGTGATAA CCATGGACGA GGACGGGGAA
       GTCACCTGGA GTTTCTTCTC CCCCACTATT GGTACCTGCT CCTGCCCCTT
6901   GAGGACGAGG ACGAGGAGGC GGAAGACCAG GAGCCCCGGG CGGCTCAGGA
       CTCCTGCTCC TGCTCCTCCG CCTTCTGGTC CTCGGGGCCC GCCGAGTCCT
6951   TCAGGGCCAA GACATAGAGA TGGTGTCCGG AGACCCCAAA AACGTCCAAG
       AGTCCCGGTT CTGTATCTCT ACCACAGGCC TCTGGGGTTT TTGCAGGTTC
7001   TTGCATTGGC TGCAAAGGGA CCCACGGTGG AACAGGAGCA GGAGCAGGAG
       AACGTAACCG ACGTTTCCCT GGGTGCCACC TTGTCCTCGT CCTCGTCCTC
7051   CGGGAGGGGC AGGAGCAGGA GGGGCAGGAG CAGGAGGAGG GGCAGGAGCA
       GCCCTCCCCG TCCTCGTCCT CCCCGTCCTC GTCCTCCTCC CCGTCCTCGT
7101   GGAGGAGGGG CAGGAGGGGC AGGAGGGGCA GGAGGGGCAG GAGCAGGAGG
       CCTCCTCCCC GTCCTCCCCG TCCTCCCCGT CCTCCCCGTC CTCGTCCTCC
7151   AGGGGCAGGA GCAGGAGGAG GGGCAGGAGG GGCAGGAGGG GCAGGAGCAG
       TCCCCGTCCT CGTCCTCCTC CCCGTCCTCC CCGTCCTCCC CGTCCTCGTC
7201   GAGGAGGGGC AGGAGCAGGA GGAGGGGCAG GAGGGGCAGG AGCAGGAGGA
       CTCCTCCCCG TCCTCGTCCT CCTCCCCGTC CTCCCCGTCC TCGTCCTCCT
7251   GGGGCAGGAG GGGCAGGAGG GGCAGGAGCA GGAGGAGGGG CAGGAGCAGG
       CCCCGTCCTC CCCGTCCTCC CCGTCCTCGT CCTCCTCCCC GTCCTCGTCC
7301   AGGAGGGGCA GGAGGGGCAG GAGCAGGAGG AGGGGCAGGA GGGGCAGGAG
       TCCTCCCCGT CCTCCCCGTC CTCGTCCTCC TCCCCGTCCT CCCCGTCCTC
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FIG. IO-8

pCEP4W/hepEK

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7351    GGGCAGGAGC AGGAGGAGGG GCAGGAGCAG GAGGGGCAGG AGGGGCAGGA
        CCCGTCCTCG TCCTCCTCCC CGTCCTCGTC CTCCCCGTCC TCCCCGTCCT
7401    GGGGCAGGAG CAGGAGGGGC AGGAGCAGGA GGAGGGGCAG GAGGGGCAGG
        CCCCGTCCTC GTCCTCCCCG TCCTCGTCCT CCTCCCCGTC CTCCCCGTCC
7451    AGGGGCAGGA GCAGGAGGGG CAGGAGCAGG AGGGGCAGGA GCAGGAGGGG
        TCCCCGTCCT CGTCCTCCCC GTCCTCGTCC TCCCCGTCCT CGTCCTCCCC
7501    CAGGAGCAGG AGGGGCAGGA GGGGCAGGAG CAGGAGGGGC AGGAGGGGCA
        GTCCTCGTCC TCCCCGTCCT CCCCGTCCTC GTCCTCCCCG TCCTCCCCGT
7551    GGAGCAGGAG GGGCAGGAGG GGCAGGAGCA GGAGGAGGGG CAGGAGGGGC
        CCTCGTCCTC CCCGTCCTCC CCGTCCTCGT CCTCCTCCCC GTCCTCCCCG
7601    AGGAGCAGGA GGAGGGGCAG GAGGGGCAGG AGCAGGAGGG GCAGGAGGGG
        TCCTCGTCCT CCTCCCCGTC CTCCCCGTCC TCGTCCTCCC CGTCCTCCCC
7651    CAGGAGCAGG AGGGGCAGGA GGGGCAGGAG CAGGAGGGGC AGGAGGGGCA
        GTCCTCGTCC TCCCCGTCCT CCCCGTCCTC GTCCTCCCCG TCCTCCCCGT
7701    GGAGCAGGAG GAGGGGCAGG AGCAGGAGGG GCAGGAGCAG GAGGTGGAGG
        CCTCGTCCTC CTCCCCGTCC TCGTCCTCCC CGTCCTCGTC CTCCACCTCC
7751    CCGGGGTCGA GGAGGCAGTG GAGGCCGGGG TCGAGGAGGT AGTGGAGGCC
        GGCCCCAGCT CCTCCGTCAC CTCCGGCCCC AGCTCCTCCA TCACCTCCGG
7801    GGGGTCGAGG AGGTAGTGGA GGCCGCCGGG GTAGAGGACG TGAAAGAGCC
        CCCCAGCTCC TCCATCACCT CCGGCGGCCC CATCTCCTGC ACTTTCTCGG
7851    AGGGGGGGAA GTCGTGAAAG AGCCAGGGGG AGAGGTCGTG GACGTGGAGA
        TCCCCCCCTT CAGCACTTTC TCGGTCCCCC TCTCCAGCAC CTGCACCTCT
7901    AAAGAGGCCC AGGAGTCCCA GTAGTCAGTC ATCATCATCC GGGTCTCCAC
        TTTCTCCGGG TCCTCAGGGT CATCAGTCAG TAGTAGTAGG CCCAGAGGTG
7951    CGCGCAGGCC CCCTCCAGGT AGAAGGCCAT TTTTCCACCC TGTAGGGGAA
        GCGCGTCCGG GGGAGGTCCA TCTTCCGGTA AAAAGGTGGG ACATCCCCTT
8001    GCCGATTATT TTGAATACCA CCAAGAAGGT GGCCCAGATG GTGAGCCTGA
        CGGCTAATAA AACTTATGGT GGTTCTTCCA CCGGGTCTAC CACTCGGACT
8051    CGTGCCCCCG GGAGCGATAG AGCAGGGCCC CGCAGATGAC CCAGGAGAAG
        GCACGGGGGC CCTCGCTATC TCGTCCCGGG GCGTCTACTG GGTCCTCTTC
8101    GCCCAAGCAC TGGACCCCGG GGTCAGGGTG ATGGAGGCAG GCGCAAAAAA
        CGGGTTCGTG ACCTGGGGCC CCAGTCCCAC TACCTCCGTC CGCGTTTTTT
8151    GGAGGGTGGT TTGGAAAGCA TCGTGGTCAA GGAGGTTCCA ACCCGAAATT
        CCTCCCACCA AACCTTTCGT AGCACCAGTT CCTCCAAGGT TGGGCTTTAA
8201    TGAGAACATT GCAGAAGGTT TAAGAGCTCT CCTGGCTAGG AGTCACGTAG
        ACTCTTGTAA CGTCTTCCAA ATTCTCGAGA GGACCGATCC TCAGTGCATC
8251    AAAGGACTAC CGACGAAGGA ACTTGGGTCG CCGGTGTGTT CGTATATGGA
        TTTCCTGATG GCTGCTTCCT TGAACCCAGC GGCCACACAA GCATATACCT
8301    GGTAGTAAGA CCTCCCTTTA CAACCTAAGG CGAGGAACTG CCCTTGCTAT
        CCATCATTCT GGAGGGAAAT GTTGGATTCC GCTCCTTGAC GGGAACGATA
8351    TCCACAATGT CGTCTTACAC CATTGAGTCG TCTCCCCTTT GGAATGGCCC
        AGGTGTTACA GCAGAATGTG GTAACTCAGC AGAGGGGAAA CCTTACCGGG
8401    CTGGACCCGG CCCACAACCT GGCCCGCTAA GGGAGTCCAT TGTCTGTTAT
        GACCTGGGCC GGGTGTTGGA CCGGGCGATT CCCTCAGGTA ACAGACAATA
8451    TTCATGGTCT TTTTACAAAC TCATATATTT GCTGAGGTTT TGAAGGATGC
        AAGTACCAGA AAAATGTTTG AGTATATAAA CGACTCCAAA ACTTCCTACG
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FIG. IO-9

pCEP4W/hepEK

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8501   GATTAAGGAC  CTTGTTATGA  CAAAGCCCGC  TCCTACCTGC  AATATCAGGG
       CTAATTCCTG  GAACAATACT  GTTTCGGGCG  AGGATGGACG  TTATAGTCCC
8551   TGACTGTGTG  CAGCTTTGAC  GATGGAGTAG  ATTTGCCTCC  CTGGTTTCCA
       ACTGACACAC  GTCGAAACTG  CTACCTCATC  TAAACGGAGG  GACCAAAGGT
8601   CCTATGGTGG  AAGGGGCTGC  CGCGGAGGGT  GATGACGGAG  ATGACGGAGA
       GGATACCACC  TTCCCCGACG  GCGCCTCCCA  CTACTGCCTC  TACTGCCTCT
8651   TGAAGGAGGT  GATGGAGATG  AGGGTGAGGA  AGGGCAGGAG  TGATGTAACT
       ACTTCCTCCA  CTACCTCTAC  TCCCACTCCT  TCCCGTCCTC  ACTACATTGA
8701   TGTTAGGAGA  CGCCCTCAAT  CGTATTAAAA  GCCGTGTATT  CCCCCGCACT
       ACAATCCTCT  GCGGGAGTTA  GCATAATTTT  CGGCACATAA  GGGGGCGTGA
8751   AAAGAATAAA  TCCCCAGTAG  ACATCATGCG  TGCTGTTGGT  GTATTTCTGG
       TTTCTTATTT  AGGGGTCATC  TGTAGTACGC  ACGACAACCA  CATAAAGACC
8801   CCATCTGTCT  TGTCACCATT  TTCGTCCTCC  CAACATGGGG  CAATTGGGCA
       GGTAGACAGA  ACAGTGGTAA  AAGCAGGAGG  GTTGTACCCC  GTTAACCCGT
8851   TACCCATGTT  GTCACGTCAC  TCAGCTCCGC  GCTCAACACC  TTCTCGCGTT
       ATGGGTACAA  CAGTGCAGTG  AGTCGAGGCG  CGAGTTGTGG  AAGAGCGCAA
8901   GGAAACATT  AGCGACATTT  ACCTGGTGAG  CAATCAGACA  TGCGACGGCT
       CCTTTTGTAA  TCGCTGTAAA  TGGACCACTC  GTTAGTCTGT  ACGCTGCCGA
8951   TTAGCCTGGC  CTCCTTAAAT  TCACCTAAGA  ATGGGAGCAA  CCAGCATGCA
       AATCGGACCG  GAGGAATTTA  AGTGGATTCT  TACCCTCGTT  GGTCGTACGT
9001   GGAAAAGGAC  AAGCAGCGAA  AATTCACGCC  CCCTTGGGAG  GTGGCGGCAT
       CCTTTTCCTG  TTCGTCGCTT  TTAAGTGCGG  GGGAACCCTC  CACCGCCGTA
9051   ATGCAAAGGA  TAGCACTCCC  ACTCTACTAC  TGGGTATCAT  ATGCTGACTG
       TACGTTTCCT  ATCGTGAGGG  TGAGATGATG  ACCCATAGTA  TACGACTGAC
9101   TATATGCATG  AGGATAGCAT  ATGCTACCCG  GATACAGATT  AGGATAGCAT
       ATATACGTAC  TCCTATCGTA  TACGATGGGC  CTATGTCTAA  TCCTATCGTA
9151   ATACTACCCA  GATATAGATT  AGGATAGCAT  ATGCTACCCA  GATATAGATT
       TATGATGGGT  CTATATCTAA  TCCTATCGTA  TACGATGGGT  CTATATCTAA
9201   AGGATAGCCT  ATGCTACCCA  GATATAAATT  AGGATAGCAT  ATACTACCCA
       TCCTATCGGA  TACGATGGGT  CTATATTTAA  TCCTATCGTA  TATGATGGGT
9251   GATATAGATT  AGGATAGCAT  ATGCTACCCA  GATATAGATT  AGGATAGCCT
       CTATATCTAA  TCCTATCGTA  TACGATGGGT  CTATATCTAA  TCCTATCGGA
9301   ATGCTACCCA  GATATAGATT  AGGATAGCAT  ATGCTACCCA  GATATAGATT
       TACGATGGGT  CTATATCTAA  TCCTATCGTA  TACGATGGGT  CTATATCTAA
9351   AGGATAGCAT  ATGCTATCCA  GATATTTGGG  TAGTATATGC  TACCCAGATA
       TCCTATCGTA  TACGATAGGT  CTATAAACCC  ATCATATACG  ATGGGTCTAT
9401   TAAATTAGGA  TAGCATATAC  TACCCTAATC  TCTATTAGGA  TAGCATATGC
       ATTTAATCCT  ATCGTATATG  ATGGGATTAG  AGATAATCCT  ATCGTATACG
9451   TACCCGGATA  CAGATTAGGA  TAGCATATAC  TACCCAGATA  TAGATTAGGA
       ATGGGCCTAT  GTCTAATCCT  ATCGTATATG  ATGGGTCTAT  ATCTAATCCT
9501   TAGCATATGC  TACCCAGATA  TAGATTAGGA  TAGCCTATGC  TACCCAGATA
       ATCGTATACG  ATGGGTCTAT  ATCTAATCCT  ATCGGATACG  ATGGGTCTAT
9551   TAAATTAGGA  TAGCATATAC  TACCCAGATA  TAGATTAGGA  TAGCATATGC
       ATTTAATCCT  ATCGTATATG  ATGGGTCTAT  ATCTAATCCT  ATCGTATACG
9601   TACCCAGATA  TAGATTAGGA  TAGCCTATGC  TACCCAGATA  TAGATTAGGA
       ATGGGTCTAT  ATCTAATCCT  ATCGGATACG  ATGGGTCTAT  ATCTAATCCT
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FIG. 10-10

pCEP4W/hepEK

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9651   TAGCATATGC TATCCAGATA TTTGGGTAGT ATATGCTACC CATGGCAACA
       ATCGTATACG ATAGGTCTAT AAACCCATCA TATACGATGG GTACCGTTGT
9701   TTAGCCCACC GTGCTCTCAG CGACCTCGTG AATATGAGGA CCAACAACCC
       AATCGGGTGG CACGAGAGTC GCTGGAGCAC TTATACTCCT GGTTGTTGGG
9751   TGTGCTTGGC GCTCAGGCGC AAGTGTGTGT AATTTGTCCT CCAGATCGCA
       ACACGAACCG CGAGTCCGCG TTCACACACA TTAAACAGGA GGTCTAGCGT
9801   GCAATCGCGC CCCTATCTTG GCCCGCCCAC CTACTTATGC AGGTATTCCC
       CGTTAGCGCG GGGATAGAAC CGGGCGGGTG GATGAATACG TCCATAAGGG
9851   CGGGGTGCCA TTAGTGGTTT TGTGGGCAAG TGGTTTGACC GCAGTGGTTA
       GCCCCACGGT AATCACCAAA ACACCCGTTC ACCAAACTGG CGTCACCAAT
9901   GCGGGGTTAC AATCAGCCAA GTTATTACAC CCTTATTTTA CAGTCCAAAA
       CGCCCCAATG TTAGTCGGTT CAATAATGTG GGAATAAAAT GTCAGGTTTT
9951   CCGCAGGGCG GCGTGTGGGG GCTGACGCGT GCCCCACTC CACAATTTCA
       GGCGTCCCGC CGCACACCCC CGACTGCGCA CGGGGGTGAG GTGTTAAAGT
10001  AAAAAAAGAG TGGCCACTTG TCTTTGTTTA TGGGCCCCAT TGGCGTGGAG
       TTTTTTTCTC ACCGGTGAAC AGAAACAAAT ACCCGGGGTA ACCGCACCTC
10051  CCCCGTTTAA TTTTCGGGGG TGTTAGAGAC AACCAGTGGA GTCCGCTGCT
       GGGGCAAATT AAAAGCCCCC ACAATCTCTG TTGGTCACCT CAGGCGACGA
10101  GTCGGCGTCC ACTCTCTTTC CCCTTGTTAC AAATAGAGTG TAACAACATG
       CAGCCGCAGG TGAGAGAAAG GGGAACAATG TTTATCTCAC ATTGTTGTAC
10151  GTTCACCTGT CTTGGTCCCT GCCTGGGACA CATCTTAATA ACCCCAGTAT
       CAAGTGGACA GAACCAGGGA CGGACCCTGT GTAGAATTAT TGGGGTCATA
10201  CATATTGCAC TAGGATTATG TGTTGCCCAT AGCCATAAAT TCGTGTGAGA
       GTATAACGTG ATCCTAATAC ACAACGGGTA TCGGTATTTA AGCACACTCT
10251  TGGACATCCA GTCTTTACGG CTTGTCCCCA CCCCATGGAT TTCTATTGTT
       ACCTGTAGGT CAGAAATGCC GAACAGGGGT GGGGTACCTA AAGATAACAA
10301  AAAGATATTC AGAATGTTTC ATTCCTACAC TAGTATTTAT TGCCCAAGGG
       TTTCTATAAG TCTTACAAAG TAAGGATGTG ATCATAAATA ACGGGTTCCC
10351  GTTTGTGAGG GTTATATTGG TGTCATAGCA CAATGCCACC ACTGAACCCC
       CAAACACTCC CAATATAACC ACAGTATCGT GTTACGGTGG TGACTTGGGG
10401  CCGTCCAAAT TTTATTCTGG GGGCGTCACC TGAAACCTTG TTTTCGAGCA
       GGCAGGTTTA AAATAAGACC CCCGCAGTGG ACTTTGGAAC AAAAGCTCGT
10451  CCTCACATAC ACCTTACTGT TCACAACTCA GCAGTTATTC TATTAGCTAA
       GGAGTGTATG TGGAATGACA AGTGTTGAGT CGTCAATAAG ATAATCGATT
10501  ACGAAGGAGA ATGAAGAAGC AGGCGAAGAT TCAGGAGAGT TCACTGCCCG
       TGCTTCCTCT TACTTCTTCG TCCGCTTCTA AGTCCTCTCA AGTGACGGGC
10551  CTCCTTGATC TTCAGCCACT GCCCTTGTGA CTAAAATGGT TCACTACCCT
       GAGGAACTAG AAGTCGGTGA CGGGAACACT GATTTTACCA AGTGATGGGA
10601  CGTGGAATCC TGACCCCATG TAAATAAAAC CGTGACAGCT CATGGGGTGG
       GCACCTTAGG ACTGGGGTAC ATTTATTTTG GCACTGTCGA GTACCCCACC
10651  GAGATATCGC TGTTCCTTAG GACCCTTTTA CTAACCCTAA TTCGATAGCA
       CTCTATAGCG ACAAGGAATC CTGGGAAAAT GATTGGGATT AAGCTATCGT
10701  TATGCTTCCC GTTGGGTAAC ATATGCTATT GAATTAGGGT TAGTCTGGAT
       ATACGAAGGG CAACCCATTG TATACGATAA CTTAATCCCA ATCAGACCTA
10751  AGTATATACT ACTACCCGGG AAGCATATGC TACCCGTTTA GGGTTAACAA
       TCATATATGA TGATGGGCCC TTCGTATACG ATGGGCAAAT CCCAATTGTT
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FIG. 10-11

pCEP4W/hepEK

10801 GGGGGCCTTA TAAACACTAT TGCTAATGCC CTCTTGAGGG TCCGCTTATC
      CCCCCGGAAT ATTTGTGATA ACGATTACGG GAGAACTCCC AGGCGAATAG

10851 GGTAGCTACA CAGGCCCCTC TGATTGACGT TGGTGTAGCC TCCCGTAGTC
      CCATCGATGT GTCCGGGGAG ACTAACTGCA ACCACATCGG AGGGCATCAG

10901 TTCCTGGGCC CCTGGGAGGT ACATGTCCCC CAGCATTGGT GTAAGAGCTT
      AAGGACCCGG GGACCCTCCA TGTACAGGGG GTCGTAACCA CATTCTCGAA

10951 CAGCCAAGAG TTACACATAA AGGCAATGTT GTGTTGCAGT CCACAGACTG
      GTCGGTTCTC AATGTGTATT TCCGTTACAA CACAACGTCA GGTGTCTGAC

11001 CAAAGTCTGC TCCAGGATGA AAGCCACTCA GTGTTGGCAA ATGTGCACAT
      GTTTCAGACG AGGTCCTACT TTCGGTGAGT CACAACCGTT TACACGTGTA

11051 CCATTTATAA GGATGTCAAC TACAGTCAGA GAACCCCTTT GTGTTTGGTC
      GGTAAATATT CCTACAGTTG ATGTCAGTCT CTTGGGGAAA CACAAACCAG

11101 CCCCCCCGTG TCACATGTGG AACAGGGCCC AGTTGGCAAG TTGTACCAAC
      GGGGGGGCAC AGTGTACACC TTGTCCCGGG TCAACCGTTC AACATGGTTG

11151 CAACTGAAGG GATTACATGC ACTGCCCCGC GAAGAAGGGG CAGAGATGCC
      GTTGACTTCC CTAATGTACG TGACGGGGCG CTTCTTCCCC GTCTCTACGG

11201 GTAGTCAGGT TTAGTTCGTC CGGCGGCGGG GCTCTAGAGT CGACCGGTCA
      CATCAGTCCA AATCAAGCAG GCCGCCGCCC CGAGATCTCA GCTGGCCAGT

11251 TGGCTGCGCC CCGACACCCG CCAACACCCG CTGACGCGCC CTGACGGGCT
      ACCGACGCGG GGCTGTGGGC GGTTGTGGGC GACTGCGCGG GACTGCCCGA

11301 TGTCTGCTCC CGGCATCCGC TTACAGACAA GCTGTGACCG TCTCCGGGAG
      ACAGACGAGG GCCGTAGGCG AATGTCTGTT CGACACTGGC AGAGGCCCTC

11351 CTGCATGTGT CAGAGGTTTT CACCGTCATC ACCGAAACGC GCGAGGCAGC
      GACGTACACA GTCTCCAAAA GTGGCAGTAG TGGCTTTGCG CGCTCCGTCG

11401 CGGATCATAA TCAGCCATAC CACATTTGTA GAGGTTTTAC TTGCTTTAAA
      GCCTAGTATT AGTCGGTATG GTGTAAACAT CTCCAAAATG AACGAAATTT

11451 AAACCTCCCC ACCTCCCCCT GAACCTGAAA CATAAAATGA ATGCAATTGT
      TTTGGAGGGG TGGAGGGGGA CTTGGACTTT GTATTTTACT TACGTTAACA

11501 TGTTGTTAAC TTGTTTATTG CAGCTTATAA TGGTTACAAA TAAAGCAATA
      ACAACAATTG AACAAATAAC GTCGAATATT ACCAATGTTT ATTTCGTTAT

11551 GCATCACAAA TTTCACAAAT AAAGCATTTT TTTCACTGCA TTCTAGTTGT
      CGTAGTGTTT AAAGTGTTTA TTTCGTAAAA AAAGTGACGT AAGATCAACA

11601 GGTTTGTCCA AACTCATCAA TGTATCTTAT CATGTCTGGA TCCCACGTGC
      CCAAACAGGT TTGAGTAGTT ACATAGAATA GTACAGACCT AGGGTGCACG

11651 AGGCGGGGAG GCGGCCCAAA GGGAGATCCG ACTCGTCTGA GGGCGAAGGC
      TCCGCCCCTC CGCCGGGTTT CCCTCTAGGC TGAGCAGACT CCCGCTTCCG

11701 GAAGACGCGG AAGAGGCCGC AGAGCCGGCA GCAGGCCGCG GGAAGGAAGG
      CTTCTGCGCC TTCTCCGGCG TCTCGGCCGT CGTCCGGCGC CCTTCCTTCC

11751 TCCGCTGGAT TGAGGGCCGA AGGGACGTAG CAGAAGGACG TCCCGCGCAG
      AGGCGACCTA ACTCCCGGCT TCCCTGCATC GTCTTCCTGC AGGGCGCGTC

11801 AATCCAGGTG GCAACACAGG CGAGCAGCCA AGGAAAGGAC GATGATTTCC
      TTAGGTCCAC CGTTGTGTCC GCTCGTCGGT TCCTTTCCTG CTACTAAAGG

11851 CCGACAACAC CACGGAATTG TCAGTGCCCA ACAGCCGAGC CCCTGTCCAG
      GGCTGTTGTG GTGCCTTAAC AGTCACGGGT TGTCGGCTCG GGACAGGTC

11901 CAGCGGGCAA GGCAGGCGGC GATGAGTTCC GCCGTGGCAA TAGGGAGGGG
      GTCGCCCGTT CCGTCCGCCG CTACTCAAGG CGGCACCGTT ATCCCTCCCC

FIG. 10-12

pCEP4W/hepEK

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11951   GAAAGCGAAA GTCCCGGAAA GGAGCTGACA GGTGGTGGCA ATGCCCCAAC
        CTTTCGCTTT CAGGGCCTTT CCTCGACTGT CCACCACCGT TACGGGGTTG
12001   CAGTGGGGGT TGCGTCAGCA AACACAGTGC ACACCACGCC ACGTTGCCTG
        GTCACCCCCA ACGCAGTCGT TTGTGTCACG TGTGGTGCGG TGCAACGGAC
12051   ACAACGGGCC ACAACTCCTC ATAAAGAGAC AGCAACCAGG ATTTATACAA
        TGTTGCCCGG TGTTGAGGAG TATTTCTCTG TCGTTGGTCC TAAATATGTT
12101   GGAGGAGAAA ATGAAAGCCA TACGGGAAGC AATAGCATGA TACAAAGGCA
        CCTCCTCTTT TACTTTCGGT ATGCCCTTCG TTATCGTACT ATGTTTCCGT
12151   TTAAAGCAGC GTATCCACAT AGCGTAAAAG GAGCAACATA GTTAAGAATA
        AATTTCGTCG CATAGGTGTA TCGCATTTTC CTCGTTGTAT CAATTCTTAT
12201   CCAGTCAATC TTTCACAAAT TTTGTAATCC AGAGGTTGAT TC
        GGTCAGTTAG AAAGTGTTTA AAACATTAGG TCTCCAACTA AG
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FIG. 11-1

pCEP4W/hep36

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  1   TCGAGCGGCC GCTTTAAACT CAATGGTGAT GGTGATGATG ACCGGTACGC
      AGCTCGCCGG CGAAATTTGA GTTACCACTA CCACTACTAC TGGCCATGCG
 -3                       H    H    H    H    H    H    G    T    R    T
 51   GTAGAATCGA GACCGAGGAG AGGGTTAGGG ATAGGCTTAC CGAATTCGAG
      CATCTTAGCT CTGGCTCCTC TCCCAATCCC TATCCGAATG GCTTAAGCTC
 -3    T   S   D   L   G   L   L   P   N   P   I   P   K   G   F   E   L
101   CTGGGTCACC ATGCCGCTGG CTTCGGAGTG AGTCTTTATG GCCTGGAAGA
      GACCCAGTGG TACGGCGACC GAAGCCTCAC TCAGAAATAC CGGACCTTCT
 -3    Q   T   V   M   G   S   A   E   S   H   T   K   I   A   Q   F   I
151   TCCACTCCCG GAAGTCACTG ACTTTGGTGT AGACGCCTGG CTTCTGGGCC
      AGGTGAGGGC CTTCAGTGAC TGAAACCACA TCTGCGGACC GAAGACCCGG
 -3    I   W   E   R   F   D   S   V   K   T   Y   V   G   P   K   Q   A   L
201   AGGGCACAGC CAGTGCCCCA ACTCACAATG CCACACAGCC GCCAACGTGG
      TCCCGTGTCG GTCACGGGGT TGAGTGTTAC GGTGTGTCGG CGGTTGCACC
 -3    L   A   C   G   T   G   W   S   V   I   G   C   L   R   W   R   P
251   CGTCCGAGAG ATGCTGTCCT CACACACAAA GGGACCACCG CTGTCGCCCT
      GCAGGCTCTC TACGACAGGA GTGTGTGTTT CCCTGGTGGC GACAGCGGGA
 -3    T   R   S   I   S   D   E   C   V   F   P   G   G   S   D   G   Q
301   GGCAGGCATC AATGCCACCC TCGGGGTAGC CAGCACAGAA CATCTTGGGC
      CCGTCCGTAG TTACGGTGGG AGCCCCATCG GTCGTGTCTT GTAGAACCCG
 -3    Q   C   A   D   I   G   G   E   P   Y   G   A   C   F   M   K   P   K
351   TTGATCTGGT TTCCATAGAA ATCAGCGCCA TTGCAGACAT CATTGCTGAT
      AACTAGACCA AAGGTATCTT TAGTCGCGGT AACGTCTGTA GTAACGACTA
 -3    K   I   Q   N   G   Y   F   D   A   G   N   C   V   D   N   S   I
401   TATGGGGACT CGAGCCTCCT GGAGTACCCC GGCCTGTTGG CCATAGTACT
      ATACCCCTGA GCTCGGAGGA CCTCATGGGG CCGGACAACC GGTATCATGA
 -3    I   P   V   R   A   E   Q   L   V   G   A   Q   Q   G   Y   Y   Q
451   GCGTGTTGCC CCAGCCCGTC ACGGTACAGA TCTTGCCATC CACCAGGGCC
      CGCACAACGG GGTCGGGCAG TGCCATGTCT AGAACGGTAG GTGGTCCCGG
 -3    Q   T   N   G   W   G   T   V   T   C   I   K   G   D   V   L   A   Q
501   TGGCCGGCAG CTGGGAGGCA CACAGGCTGG ATGTATTCTG TGAGGGGCAG
      ACCGGCCGTC GACCCTCCGT GTGTCCGACC TACATAAGAC ACTCCCCGTC
 -3    Q   G   A   A   P   L   C   V   P   Q   I   Y   E   T   L   P   L
551   GGGACTGGAG AGGTGGACCA GGGCAATATC GTTGCTGTTC TCCTCGCTGT
      CCCTGACCTC TCCACCTGGT CCCGTTATAG CAACGACAAG AGGAGCGACA
 -3    P   S   S   L   H   V   L   A   I   D   N   S   N   E   E   S   N
601   TGGGGTCCCG AAAGGGAAGA TAGCCCCCGT GGTAGACCAC AGCCTGCACC
      ACCCCAGGGC TTTCCCTTCT ATCGGGGGCA CCATCTGGTG TCGGACGTGG
 -3    N   P   D   R   F   P   L   Y   G   G   H   Y   V   V   A   Q   V   G
651   CCCAGCTGCA GACCGTGGGG AGAGGCCTGG GCCACGGCAC CGGCAAACAC
      GGGTCGACGT CTGGCACCCC TCTCCGGACC CGGTGCCGTG GCCGTTTGTG
 -3    G   L   Q   L   G   H   P   S   A   Q   A   V   A   G   A   F   V
701   TCGCCATCGG GACAGGACCC GGTTCCGCTC CGGGAAGCAG TGGGCGGCTG
      AGCGGTAGCC CTGTCCTGGG CCAAGGCGAG GCCCTTCGTC ACCCGCCGAC
 -3    R   W   R   S   L   V   R   N   R   E   P   F   C   H   A   A   T
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FIG. 11-2

pCEP4W/hep36

```
 751  TCAGCACCCA GTCCCCGGAG AGCAGGGATC CCCCACAGAG GTGTGCTCCA .
       AGTCGTGGGT CAGGGGCCTC TCGTCCCTAG GGGGTGTCTC CACACGAGGT
  -3    ·T  L   V   W   D   G   S   L   L   S   G   G   C   L   H   A   G   D
 801  TCATAGCGAA GGCTGACTTG CCACGGCCAC CGGCCCAAGC TGGTGTCCCG
       AGTATCGCTT CCGACTGAAC GGTGCCGGTG GCCGGGTTCG ACCACAGGGC
  -3    ·D  Y   R   L   S   V   Q   W   P   W   R   G   L   S   T   D   R
 851  GCCTCCCACG ATCTTGTCGT CGTCGTCCAC GGGCAGCTTC CTGCGGCCAC
       CGGAGGGTGC TAGAACAGCA GCAGCAGGTG CCCGTCGAAG GACGCCGGTG
  -3    G   G   V   I   K   D   D   D   D   V   P   L   K   R   R   G   C·
 901  AGTCTTGGTC CGGAGCGTCA CCAGTGGAAC CTGGAACCCA GAGCAGCAGT
       TCAGAACCAG GCCTCGCAGT GGTCACCTTG GACCTTGGGT CTCGTCGTCA
  -3    ·C  D   Q   D   P   A   D   G   T   S   G   P   V   W   L   L   L   V
 951  ACCCATAGCA GGAGTGTGTC TGTCTCCATG GTGGCGATCT GGTACCCAGC
       TGGGTATCGT CCTCACACAG ACAGAGGTAC CACCGCTAGA CCATGGGTCG
  -3    ·V  W   L   L   L   T   D   T   E   M
1001  TTCTAGAGAT CTGACGGTTC ACTAAACGAG CTCTGCTTAT ATAGACCTCC
       AAGATCTCTA GACTGCCAAG TGATTTGCTC GAGACGAATA TATCTGGAGG
1051  CACCGTACAC GCCTACCGCC CATTTGCGTC AACGGGGCGG GGTTATTACG
       GTGGCATGTG CGGATGGCGG GTAAACGCAG TTGCCCCGCC CCAATAATGC
1101  ACATTTTGGA AAGTCCCGTT GATTTTGGTG CCAAAACAAA CTCCCATTGA
       TGTAAAACCT TTCAGGGCAA CTAAAACCAC GGTTTTGTTT GAGGGTAACT
1151  CGTCAATGGG GTGGAGACTT GGAAATCCCC GTGAGTCAAA CCGCTATCCA
       GCAGTTACCC CACCTCTGAA CCTTTAGGGG CACTCAGTTT GGCGATAGGT
1201  CGCCCATTGG TGTACTGCCA AAACCGCATC ACCATGGTAA TAGCGATGAC
       GCGGGTAACC ACATGACGGT TTTGGCGTAG TGGTACCATT ATCGCTACTG
1251  TAATACGTAG ATGTACTGCC AAGTAGGAAA GTCCCGTAAG GTCATGTACT
       ATTATGCATC TACATGACGG TTCATCCTTT CAGGGCATTC CAGTACATGA
1301  GGGCATAATG CCAGGCGGGC CATTTACCGT CATTGACGTC AATAGGGGGC
       CCCGTATTAC GGTCCGCCCG GTAAATGGCA GTAACTGCAG TTATCCCCCG
1351  GGACTTGGCA TATGATACAC TTGATGTACT GCCAAGTGGG CAGTTTACCG
       CCTGAACCGT ATACTATGTG AACTACATGA CGGTTCACCC GTCAAATGGC
1401  TAAATACTCC ACCCATTGAC GTCAATGGAA AGTCCCTATT GGCGTTACTA
       ATTTATGAGG TGGGTAACTG CAGTTACCTT TCAGGGATAA CCGCAATGAT
1451  TGGGAACATA CGTCATTATT GACGTCAATG GGCGGGGGTC GTTGGGCGGT
       ACCCTTGTAT GCAGTAATAA CTGCAGTTAC CCGCCCCCAG CAACCCGCCA
1501  CAGCCAGGCG GGCCATTTAC CGTAAGTTAT GTAACGCGGA ACTCCATATA
       GTCGGTCCGC CCGGTAAATG GCATTCAATA CATTGCGCCT TGAGGTATAT
1551  TGGGCTATGA ACTAATGACC CCGTAATTGA TTACTATTAA TAACTAGTCA
       ACCCGATACT TGATTACTGG GGCATTAACT AATGATAATT ATTGATCAGT
1601  ATAATCAATG TCAACATGGC GGTCATATTG GACATGAGCC AATATAAATG
       TATTAGTTAC AGTTGTACCG CCAGTATAAC CTGTACTCGG TTATATTTAC
1651  TACATATTAT GATATAGATA CAACGTATGC AATGGCCAAT AGCCAATATT
       ATGTATAATA CTATATCTAT GTTGCATACG TTACCGGTTA TCGGTTATAA
1701  GATTTATGCT ATATAACCAA TGACTAATAT GGCTAATTGC CAATATTGAT
       CTAAATACGA TATATTGGTT ACTGATTATA CCGATTAACG GTTATAACTA
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FIG. II-3

pCEP4W/hep36

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1751  TCAATGTATA GATCTTCCAT ACCTACCAGT TCTGCGCCTG CAGCAATGCA
      AGTTACATAT CTAGAAGGTA TGGATGGTCA AGACGCGGAC GTCGTTACGT
1801  ACAACGTTGC CCGGATCTGC GATGATAAGC TGTCAAACAT GAGAATTGGT
      TGTTGCAACG GGCCTAGACG CTACTATTCG ACAGTTTGTA CTCTTAACCA
1851  CGACTAGCTT GGCACGCCAG AAATCCGCGC GGTGGTTTTT GGGGGTCGGG
      GCTGATCGAA CCGTGCGGTC TTTAGGCGCG CCACCAAAAA CCCCCAGCCC
1901  GGTGTTTGGC AGCCACAGAC GCCCGGTGTT CGTGTCGCGC CAGTACATGC
      CCACAAACCG TCGGTGTCTG CGGGCCACAA GCACAGCGCG GTCATGTACG
1951  GGTCCATGCC CAGGCCATCC AAAAACCATG GGTCTGTCTG CTCAGTCCAG
      CCAGGTACGG GTCCGGTAGG TTTTTGGTAC CCAGACAGAC GAGTCAGGTC
2001  TCGTGGACCA GACCCCACGC AACGCCCAAA ATAATAACCC CCACGAACCA
      AGCACCTGGT CTGGGGTGCG TTGCGGGTTT TATTATTGGG GGTGCTTGGT
2051  TAAACCATTC CCCATGGGGG ACCCCGTCCC TAACCCACGG GGCCAGTGGC
      ATTTGGTAAG GGGTACCCCC TGGGGCAGGG ATTGGGTGCC CCGGTCACCG
2101  TATGGCAGGG CCTGCCGCCC CGACGTTGGC TGCGAGCCCT GGGCCTTCAC
      ATACCGTCCC GGACGGCGGG GCTGCAACCG ACGCTCGGGA CCCGGAAGTG
2151  CCGAACTTGG GGGGTGGGGT GGGGAAAAGG AAGAAACGCG GGCGTATTGG
      GGCTTGAACC CCCCACCCCA CCCCTTTTCC TTCTTTGCGC CCGCATAACC
2201  CCCCAATGGG GTCTCGGTGG GGTATCGACA GAGTGCCAGC CCTGGGACCG
      GGGGTTACCC CAGAGCCACC CCATAGCTGT CTCACGGTCG GGACCCTGGC
2251  AACCCCGCGT TTATGAACAA ACGACCCAAC ACCCGTGCGT TTTATTCTGT
      TTGGGGCGCA AATACTTGTT TGCTGGGTTG TGGGCACGCA AAATAAGACA
2301  CTTTTTATTG CCGTCATAGC GCGGGTTCCT TCCGGTATTG TCTCCTTCCG
      GAAAAATAAC GGCAGTATCG CGCCCAAGGA AGGCCATAAC AGAGGAAGGC
2351  TGTTTCAGTT AGCCTCCCCC ATCTCCCCTA TTCCTTTGCC CTCGGACGAG
      ACAAAGTCAA TCGGAGGGGG TAGAGGGGAT AAGGAAACGG GAGCCTGCTC
2401  TGCTGGGGCG TCGGTTTCCA CTATCGGCGA GTACTTCTAC ACAGCCATCG
      ACGACCCCGC AGCCAAAGGT GATAGCCGCT CATGAAGATG TGTCGGTAGC
2451  GTCCAGACGG CCGCGCTTCT GCGGGCGATT TGTGTACGCC CGACAGTCCC
      CAGGTCTGCC GGCGCGAAGA CGCCCGCTAA ACACATGCGG GCTGTCAGGG
2501  GGCTCCGGAT CGGACGATTG CGTCGCATCG ACCCTGCGCC CAAGCTGCAT
      CCGAGGCCTA GCCTGCTAAC GCAGCGTAGC TGGGACGCGG GTTCGACGTA
2551  CATCGAAATT GCCGTCAACC AAGCTCTGAT AGAGTTGGTC AAGACCAATG
      GTAGCTTTAA CGGCAGTTGG TTCGAGACTA TCTCAACCAG TTCTGGTTAC
2601  CGGAGCATAT ACGCCCGGAG CCGCGGCGAT CCTGCAAGCT CCGGATGCCT
      GCCTCGTATA TGCGGGCCTC GGCGCCGCTA GGACGTTCGA GGCCTACGGA
2651  CCGCTCGAAG TAGCGCGTCT GCTGCTCCAT ACAAGCCAAC CACGGCCTCC
      GGCGAGCTTC ATCGCGCAGA CGACGAGGTA TGTTCGGTTG GTGCCGGAGG
2701  AGAAGAAGAT GTTGGCGACC TCGTATTGGG AATCCCCGAA CATCGCCTCG
      TCTTCTTCTA CAACCGCTGG AGCATAACCC TTAGGGGCTT GTAGCGGAGC
2751  CTCCAGTCAA TGACCGCTGT TATGCGGCCA TTGTCCGTCA GGACATTGTT
      GAGGTCAGTT ACTGGCGACA ATACGCCGGT AACAGGCAGT CCTGTAACAA
2801  GGAGCCGAAA TCCGCGTGCA CGAGGTGCCG GACTTCGGGG CAGTCCTCGG
      CCTCGGCTTT AGGCGCACGT GCTCCACGGC CTGAAGCCCC GTCAGGAGCC
2851  CCCAAAGCAT CAGCTCATCG AGAGCCTGCG CGACGGACGC ACTGACGGTG
      GGGTTTCGTA GTCGAGTAGC TCTCGGACGC GCTGCCTGCG TGACTGCCAC
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FIG. 11-4

pCEP4W/hep36

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2901   TCGTCCATCA CAGTTTGCCA GTGATACACA TGGGGATCAG CAATCGCGCA
       AGCAGGTAGT GTCAAACGGT CACTATGTGT ACCCCTAGTC GTTAGCGCGT
2951   TATGAAATCA CGCCATGTAG TGTATTGACC GATTCCTTGC GGTCCGAATG
       ATACTTTAGT GCGGTACATC ACATAACTGG CTAAGGAACG CCAGGCTTAC
3001   GGCCGAACCC GCTCGTCTGG CTAAGATCGG CCGCAGCGAT CGCATCCATG
       CCGGCTTGGG CGAGCAGACC GATTCTAGCC GGCGTCGCTA GCGTAGGTAC
3051   GCCTCCGCGA CCGGCTGCAG AACAGCGGGC AGTTCGGTTT CAGGCAGGTC
       CGGAGGCGCT GGCCGACGTC TTGTCGCCCG TCAAGCCAAA GTCCGTCCAG
3101   TTGCAACGTG ACACCCTGTG CACGGCGGGA GATGCAATAG GTCAGGCTCT
       AACGTTGCAC TGTGGGACAC GTGCCGCCCT CTACGTTATC CAGTCCGAGA
3151   CGCTGAATTC CCCAATGTCA AGCACTTCCG GAATCGGGAG CGCGGCCGAT
       GCGACTTAAG GGGTTACAGT TCGTGAAGGC CTTAGCCCTC GCGCCGGCTA
3201   GCAAAGTGCC GATAAACATA ACGATCTTTG TAGAAACCAT CGGCGCAGCT
       CGTTTCACGG CTATTTGTAT TGCTAGAAAC ATCTTTGGTA GCCGCGTCGA
3251   ATTTACCCGC AGGACATATC CACGCCCTCC TACATCGAAG CTGAAAGCAC
       TAAATGGGCG TCCTGTATAG GTGCGGGAGG ATGTAGCTTC GACTTTCGTG
3301   GAGATTCTTC GCCCTCCGAG AGCTGCATCA GGTCGGAGAC GCTGTCGAAC
       CTCTAAGAAG CGGGAGGCTC TCGACGTAGT CCAGCCTCTG CGACAGCTTG
3351   TTTTCGATCA GAAACTTCTC GACAGACGTC GCGGTGAGTT CAGGCTTTTT
       AAAAGCTAGT CTTTGAAGAG CTGTCTGCAG CGCCACTCAA GTCCGAAAAA
3401   CATATCTCAT TGCCCGGGAT CTGCGGCACG CTGTTGACGC TGTTAAGCGG
       GTATAGAGTA ACGGGCCCTA GACGCCGTGC GACAACTGCG ACAATTCGCC
3451   GTCGCTGCAG GGTCGCTCGG TGTTCGAGGC CACACGCGTC ACCTTAATAT
       CAGCGACGTC CCAGCGAGCC ACAAGCTCCG GTGTGCGCAG TGGAATTATA
3501   GCGAAGTGGA CCTGGGACCG CGCCGCCCCG ACTGCATCTG CGTGTTCGAA
       CGCTTCACCT GGACCCTGGC GCGGCGGGGC TGACGTAGAC GCACAAGCTT
3551   TTCGCCAATG ACAAGACGCT GGGCGGGGTT TGTGTCATCA TAGAACTAAA
       AAGCGGTTAC TGTTCTGCGA CCCGCCCCAA ACACAGTAGT ATCTTGATTT
3601   GACATGCAAA TATATTTCTT CCGGGGACAC CGCCAGCAAA CGCGAGCAAC
       CTGTACGTTT ATATAAAGAA GGCCCCTGTG GCGGTCGTTT GCGCTCGTTG
3651   GGGCCACGGG GATGAAGCAG GGCATGGCGG CCGACGCGCT GGGCTACGTC
       CCCGGTGCCC CTACTTCGTC CCGTACCGCC GGCTGCGCGA CCCGATGCAG
3701   TTGCTGGCGT TCGCGACGCG AGGCTGGATG GCCTTCCCCA TTATGATTCT
       AACGACCGCA AGCGCTGCGC TCCGACCTAC CGGAAGGGGT AATACTAAGA
3751   TCTCGCTTCC GGCGGCATCG GGATGCCCGC GTTGCAGGCC ATGCTGTCCA
       AGAGCGAAGG CCGCCGTAGC CCTACGGGCG CAACGTCCGG TACGACAGGT
3801   GGCAGGTAGA TGACGACCAT CAGGGACAGC TTCAAGGATC GCTCGCGGCT
       CCGTCCATCT ACTGCTGGTA GTCCCTGTCG AAGTTCCTAG CGAGCGCCGA
3851   CTTACCAGCC TAACTTCGAT CACTGGACCG CTGATCGTCA CGGCGATTTA
       GAATGGTCGG ATTGAAGCTA GTGACCTGGC GACTAGCAGT GCCGCTAAAT
3901   TGCCGCCTCG GCGAGCACAT GGAACGGGTT GGCATGGATT GTAGGCGCCG
       ACGGCGGAGC CGCTCGTGTA CCTTGCCCAA CCGTACCTAA CATCCGCGGC
3951   CCCTATACCT TGTCTGCCTC CCGCGTTGC GTCGCGGTGC ATGGAGCCGG
       GGGATATGGA ACAGACGGAG GGGCGCAACG CAGCGCCACG TACCTCGGCC
4001   GCCACCTCGA CCTGAATGGA AGCCGGCGGC ACCTCGCTAA CGGATTCACC
       CGGTGGAGCT GGACTTACCT TCGGCCGCCG TGGAGCGATT GCCTAAGTGG
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FIG. II-5

pCEP4W/hep36

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4051  ACTCCAAGAA TTGGAGCCAA TCAATTCTTG CGGAGAACTG TGAATGCGCA
      TGAGGTTCTT AACCTCGGTT AGTTAAGAAC GCCTCTTGAC ACTTACGCGT
4101  AACCAACCCT TGGCAGAACA TATCCATCGC GTCCGCCATC TCCAGCAGCC
      TTGGTTGGGA ACCGTCTTGT ATAGGTAGCG CAGGCGGTAG AGGTCGTCGG
4151  GCACGCGGCG CAGCAAAAGG CCAGGAACCG TAAAAAGGCC GCGTTGCTGG
      CGTGCGCCGC GTCGTTTTCC GGTCCTTGGC ATTTTTCCGG CGCAACGACC
4201  CGTTTTTCCA TAGGCTCCGC CCCCCTGACG AGCATCACAA AAATCGACGC
      GCAAAAAGGT ATCCGAGGCG GGGGGACTGC TCGTAGTGTT TTTAGCTGCG
4251  TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGCGTT
      AGTTCAGTCT CCACCGCTTT GGGCTGTCCT GATATTTCTA TGGTCCGCAA
4301  TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA
      AGGGGGACCT TCGAGGGAGC ACGCGAGAGG ACAAGGCTGG GACGGCGAAT
4351  CCGGATACCT GTCCGCCTTT CTCCCTTCGG GAAGCGTGGC GCTTTCTCAT
      GGCCTATGGA CAGGCGGAAA GAGGGAAGCC CTTCGCACCG CGAAAGAGTA
4401  AGCTCACGCT GTAGGTATCT CAGTTCGGTG TAGGTCGTTC GCTCCAAGCT
      TCGAGTGCGA CATCCATAGA GTCAAGCCAC ATCCAGCAAG CGAGGTTCGA
4451  GGGCTGTGTG CACGAACCCC CCGTTCAGCC CGACCGCTGC GCCTTATCCG
      CCCGACACAC GTGCTTGGGG GGCAAGTCGG GCTGGCGACG CGGAATAGGC
4501  GTAACTATCG TCTTGAGTCC AACCCGGTAA GACACGACTT ATCGCCACTG
      CATTGATAGC AGAACTCAGG TTGGGCCATT CTGTGCTGAA TAGCGGTGAC
4551  GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC
      CGTCGTCGGT GACCATTGTC CTAATCGTCT CGCTCCATAC ATCCGCCACG
4601  TACAGAGTTC TTGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGGACAG
      ATGTCTCAAG AACTTCACCA CCGGATTGAT GCCGATGTGA TCTTCCTGTC
4651  TATTTGGTAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAGAGTT
      ATAAACCATA GACGCGAGAC GACTTCGGTC AATGGAAGCC TTTTTCTCAA
4701  GGTAGCTCTT GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT
      CCATCGAGAA CTAGGCCGTT TGTTTGGTGG CGACCATCGC CACCAAAAAA
4751  TGTTTGCAAG CAGCAGATTA CGCGCAGAAA AAAAGGATCT CAAGAAGATC
      ACAAACGTTC GTCGTCTAAT GCGCGTCTTT TTTTCCTAGA GTTCTTCTAG
4801  CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGAACGA AAACTCACGT
      GAAACTAGAA AAGATGCCCC AGACTGCGAG TCACCTTGCT TTTGAGTGCA
4851  TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT
      ATTCCCTAAA ACCAGTACTC TAATAGTTTT TCCTAGAAGT GGATCTAGGA
4901  TTTAAATTAA AAATGAAGTT TTAAATCAAT CTAAAGTATA TATGAGTAAA
      AAATTTAATT TTTACTTCAA AATTTAGTTA GATTTCATAT ATACTCATTT
4951  CTTGGTCTGA CAGTTACCAA TGCTTAATCA GTGAGGCACC TATCTCAGCG
      GAACCAGACT GTCAATGGTT ACGAATTAGT CACTCCGTGG ATAGAGTCGC
5001  ATCTGTCTAT TTCGTTCATC CATAGTTGCC TGACTCCCCG TCGTGTAGAT
      TAGACAGATA AAGCAAGTAG GTATCAACGG ACTGAGGGGC AGCACATCTA
5051  AACTACGATA CGGGAGGGCT TACCATCTGG CCCCAGTGCT GCAATGATAC
      TTGATGCTAT GCCCTCCCGA ATGGTAGACC GGGGTCACGA CGTTACTATG
5101  CGCGAGACCC ACGCTCACCG GCTCCAGATT TATCAGCAAT AAACCAGCCA
      GCGCTCTGGG TGCGAGTGGC CGAGGTCTAA ATAGTCGTTA TTTGGTCGGT
5151  GCCGGAAGGG CCGAGCGCAG AAGTGGTCCT GCAACTTTAT CCGCCTCCAT
      CGGCCTTCCC GGCTCGCGTC TTCACCAGGA CGTTGAAATA GGCGGAGGTA
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FIG. II-6

pCEP4W/hep36

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5201   CCAGTCTATT AATTGTTGCC GGGAAGCTAG AGTAAGTAGT TCGCCAGTTA
       GGTCAGATAA TTAACAACGG CCCTTCGATC TCATTCATCA AGCGGTCAAT
5251   ATAGTTTGCG CAACGTTGTT GCCATTGCTG CAGGCATCGT GGTGTCACGC
       TATCAAACGC GTTGCAACAA CGGTAACGAC GTCCGTAGCA CCACAGTGCG
5301   TCGTCGTTTG GTATGGCTTC ATTCAGCTCC GGTTCCCAAC GATCAAGGCG
       AGCAGCAAAC CATACCGAAG TAAGTCGAGG CCAAGGGTTG CTAGTTCCGC
5351   AGTTACATGA TCCCCCATGT TGTGCAAAAA AGCGGTTAGC TCCTTCGGTC
       TCAATGTACT AGGGGGTACA ACACGTTTTT TCGCCAATCG AGGAAGCCAG
5401   CTCCGATCGT TGTCAGAAGT AAGTTGGCCG CAGTGTTATC ACTCATGGTT
       GAGGCTAGCA ACAGTCTTCA TTCAACCGGC GTCACAATAG TGAGTACCAA
5451   ATGGCAGCAC TGCATAATTC TCTTACTGTC ATGCCATCCG TAAGATGCTT
       TACCGTCGTG ACGTATTAAG AGAATGACAG TACGGTAGGC ATTCTACGAA
5501   TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA TAGTGTATGC
       AAGACACTGA CCACTCATGA GTTGGTTCAG TAAGACTCTT ATCACATACG
5551   GGCGACCGAG TTGCTCTTGC CCGGCGTCAA CACGGGATAA TACCGCGCCA
       CCGCTGGCTC AACGAGAACG GGCCGCAGTT GTGCCCTATT ATGGCGCGGT
5601   CATAGCAGAA CTTTAAAAGT GCTCATCATT GGAAAACGTT CTTCGGGGCG
       GTATCGTCTT GAAATTTTCA CGAGTAGTAA CCTTTTGCAA GAAGCCCGC
5651   AAAACTCTCA AGGATCTTAC CGCTGTTGAG ATCCAGTTCG ATGTAACCCA
       TTTTGAGAGT TCCTAGAATG GCGACAACTC TAGGTCAAGC TACATTGGGT
5701   CTCGTGCACC CAACTGATCT TCAGCATCTT TTACTTTCAC CAGCGTTTCT
       GAGCACGTGG GTTGACTAGA AGTCGTAGAA AATGAAAGTG GTCGCAAAGA
5751   GGGTGAGCAA AAACAGGAAG GCAAAATGCC GCAAAAAAGG GAATAAGGGC
       CCCACTCGTT TTTGTCCTTC CGTTTTACGG CGTTTTTTCC CTTATTCCCG
5801   GACACGGAAA TGTTGAATAC TCATACTCTT CCTTTTTCAA TATTATTGAA
       CTGTGCCTTT ACAACTTATG AGTATGAGAA GGAAAAAGTT ATAATAACTT
5851   GCATTTATCA GGGTTATTGT CTCATGAGCG GATACATATT TGAATGTATT
       CGTAAATAGT CCCAATAACA GAGTACTCGC CTATGTATAA ACTTACATAA
5901   TAGAAAAATA AACAAATAGG GGTTCCGCGC ACATTTCCCC GAAAAGTGCC
       ATCTTTTTAT TTGTTTATCC CCAAGGCGCG TGTAAAGGGG CTTTTCACGG
5951   ACCTGACGTC TAAGAAACCA TTATTATCAT GACATTAACC TATAAAAATA
       TGGACTGCAG ATTCTTTGGT AATAATAGTA CTGTAATTGG ATATTTTTAT
6001   GGCGTATCAC GAGGCCCTTT CGTCTTCAAG AATTCTCATG TTTGACAGCT
       CCGCATAGTG CTCCGGGAAA GCAGAAGTTC TTAAGAGTAC AAACTGTCGA
6051   TATCATCGAT AAGCTGATCC TCACAGGCCG CACCCAGCTT TTCTTCCGTT
       ATAGTAGCTA TTCGACTAGG AGTGTCCGGC GTGGGTCGAA AAGAAGGCAA
6101   GCCCCAGTAG CATCTCTGTC TGGTGACCTT GAAGAGGAAG AGGAGGGGTC
       CGGGGTCATC GTAGAGACAG ACCACTGGAA CTTCTCCTTC TCCTCCCCAG
6151   CCGAGAATCC CCATCCCTAC CGTCCAGCAA AAAGGGGGAC GAGGAATTTG
       GGCTCTTAGG GGTAGGGATG GCAGGTCGTT TTTCCCCCTG CTCCTTAAAC
6201   AGGCCTGGCT TGAGGCTCAG GACGCAAATC TTGAGGATGT TCAGCGGGAG
       TCCGGACCGA ACTCCGAGTC CTGCGTTTAG AACTCCTACA AGTCGCCCTC
6251   TTTTCCGGGC TGCGAGTAAT TGGTGATGAG GACGAGGATG GTTCGGAGGA
       AAAAGGCCCG ACGCTCATTA ACCACTACTC CTGCTCCTAC CAAGCCTCCT
6301   TGGGGAATTT TCAGACCTGG ATCTGTCTGA CAGCGACCAT GAAGGGGATG
       ACCCCTTAAA AGTCTGGACC TAGACAGACT GTCGCTGGTA CTTCCCCTAC
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FIG. 11-7

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6351    AGGGTGGGGG GGCTGTTGGA GGGGGCAGGA GTCTGCACTC CCTGTATTCA
        TCCCACCCCC CCGACAACCT CCCCCGTCCT CAGACGTGAG GGACATAAGT
6401    CTGAGCGTCG TCTAATAAAG ATGTCTATTG ATCTCTTTTA GTGTGAATCA
        GACTCGCAGC AGATTATTTC TACAGATAAC TAGAGAAAAT CACACTTAGT
6451    TGTCTGACGA GGGGCCAGGT ACAGGACCTG GAAATGGCCT AGGAGAGAAG
        ACAGACTGCT CCCCGGTCCA TGTCCTGGAC CTTTACCGGA TCCTCTCTTC
6501    GGAGACACAT CTGGACCAGA AGGCTCCGGC GGCAGTGGAC CTCAAAGAAG
        CCTCTGTGTA GACCTGGTCT TCCGAGGCCG CCGTCACCTG GAGTTTCTTC
6551    AGGGGGTGAT AACCATGGAC GAGGACGGGG AAGAGGACGA GGACGAGGAG
        TCCCCCACTA TTGGTACCTG CTCCTGCCCC TTCTCCTGCT CCTGCTCCTC
6601    GCGGAAGACC AGGAGCCCCG GCGGCTCAG GATCAGGGCC AAGACATAGA
        CGCCTTCTGG TCCTCGGGGC CCGCCGAGTC CTAGTCCCGG TTCTGTATCT
6651    GATGGTGTCC GGAGACCCCA AAAACGTCCA AGTTGCATTG GCTGCAAAGG
        CTACCACAGG CCTCTGGGGT TTTTGCAGGT TCAACGTAAC CGACGTTTCC
6701    GACCCACGGT GGAACAGGAG CAGGAGCAGG AGCGGGAGGG GCAGGAGCAG
        CTGGGTGCCA CCTTGTCCTC GTCCTCGTCC TCGCCCTCCC CGTCCTCGTC
6751    GAGGGGCAGG AGCAGGAGGA GGGGCAGGAG CAGGAGGAGG GGCAGGAGGG
        CTCCCCGTCC TCGTCCTCCT CCCCGTCCTC GTCCTCCTCC CCGTCCTCCC
6801    GCAGGAGGGG CAGGAGGGGC AGGAGCAGGA GGAGGGGCAG GAGCAGGAGG
        .CGTCCTCCCC GTCCTCCCCG TCCTCGTCCT CCTCCCCGTC CTCGTCCTCC
6851    AGGGGCAGGA GGGGCAGGAG GGGCAGGAGC AGGAGGAGGG GCAGGAGCAG
        TCCCCGTCCT CCCCGTCCTC CCCGTCCTCG TCCTCCTCCC CGTCCTCGTC
6901    GAGGAGGGGC AGGAGGGGCA GGAGCAGGAG GAGGGGCAGG AGGGGCAGGA
        CTCCTCCCCG TCCTCCCCGT CCTCGTCCTC CTCCCCGTCC TCCCCGTCCT
6951    GGGGCAGGAG CAGGAGGAGG GGCAGGAGCA GGAGGAGGGG CAGGAGGGGC
        .CCCCGTCCTC GTCCTCCTCC CCGTCCTCGT CCTCCTCCCC GTCCTCCCCG
7001    AGGAGCAGGA GGAGGGGCAG GAGGGGCAGG AGGGGCAGGA GCAGGAGGAG
        TCCTCGTCCT CCTCCCCGTC CTCCCCGTCC TCCCCGTCCT CGTCCTCCTC
7051    GGGCAGGAGC AGGAGGGGCA GGAGGGGCAG GAGGGGCAGG AGCAGGAGGG
        CCCGTCCTCG TCCTCCCCGT CCTCCCCGTC CTCCCCGTCC TCGTCCTCCC
7101    GCAGGAGCAG GAGGAGGGGC AGGAGGGGCA GGAGGGGCAG GAGCAGGAGG
        CGTCCTCGTC CTCCTCCCCG TCCTCCCCGT CCTCCCCGTC CTCGTCCTCC
7151    GGCAGGAGCA GGAGGGGCAG GAGCAGGAGG GGCAGGAGCA GGAGGGGCAG
        CCGTCCTCGT CCTCCCCGTC CTCGTCCTCC CCGTCCTCGT CCTCCCCGTC
7201    GAGGGGCAGG AGCAGGAGGG GCAGGAGGGG CAGGAGCAGG AGGGGCAGGA
        CTCCCCGTCC TCGTCCTCCC CGTCCTCCCC GTCCTCGTCC TCCCCGTCCT
7251    GGGGCAGGAG CAGGAGGAGG GGCAGGAGGG GCAGGAGCAG GAGGAGGGGC
        CCCCGTCCTC GTCCTCCTCC CCGTCCTCCC CGTCCTCGTC CTCCTCCCCG
7301    AGGAGGGGCA GGAGCAGGAG GGGCAGGAGG GGCAGGAGCA GGAGGGGCAG
        TCCTCCCCGT CCTCGTCCTC CCCGTCCTCC CCGTCCTCGT CCTCCCCGTC
7351    GAGGGGCAGG AGCAGGAGGG GCAGGAGGGG CAGGAGCAGG AGGAGGGGCA
        CTCCCCGTCC TCGTCCTCCC CGTCCTCCCC GTCCTCGTCC TCCTCCCCGT
7401    GGAGCAGGAG GGGCAGGAGC AGGAGGTGGA GGCCGGGGTC GAGGAGGCAG
        CCTCGTCCTC CCCGTCCTCG TCCTCCACCT CCGGCCCCAG CTCCTCCGTC
7451    TGGAGGCCGG GGTCGAGGAG GTAGTGGAGG CCGGGGTCGA GGAGGTAGTG
        ACCTCCGGCC CCAGCTCCTC CATCACCTCC GGCCCCAGCT CCTCCATCAC
```

FIG. 11-8

pCEP4W/hep36

```
7501   GAGGCCGCCG GGGTAGAGGA CGTGAAAGAG CCAGGGGGGG AAGTCGTGAA
       CTCCGGCGGC CCCATCTCCT GCACTTTCTC GGTCCCCCCC TTCAGCACTT

7551   AGAGCCAGGG GGAGAGGTCG TGGACGTGGA GAAAAGAGGC CCAGGAGTCC
       TCTCGGTCCC CCTCTCCAGC ACCTGCACCT CTTTTCTCCG GGTCCTCAGG

7601   CAGTAGTCAG TCATCATCAT CCGGGTCTCC ACCGCGCAGG CCCCCTCCAG
       GTCATCAGTC AGTAGTAGTA GGCCCAGAGG TGGCGCGTCC GGGGGAGGTC

7651   GTAGAAGGCC ATTTTTCCAC CCTGTAGGGG AAGCCGATTA TTTTGAATAC
       CATCTTCCGG TAAAAAGGTG GGACATCCCC TTCGGCTAAT AAAACTTATG

7701   CACCAAGAAG GTGGCCCAGA TGGTGAGCCT GACGTGCCCC CGGGAGCGAT
       GTGGTTCTTC CACCGGGTCT ACCACTCGGA CTGCACGGGG GCCCTCGCTA

7751   AGAGCAGGGC CCCGCAGATG ACCCAGGAGA AGGCCCAAGC ACTGGACCCC
       TCTCGTCCCG GGGCGTCTAC TGGGTCCTCT TCCGGGTTCG TGACCTGGGG

7801   GGGGTCAGGG TGATGGAGGC AGGCGCAAAA AAGGAGGGTG GTTTGGAAAG
       CCCCAGTCCC ACTACCTCCG TCCGCGTTTT TTCCTCCCAC CAAACCTTTC

7851   CATCGTGGTC AAGGAGGTTC CAACCCGAAA TTTGAGAACA TTGCAGAAGG
       GTAGCACCAG TTCCTCCAAG GTTGGGCTTT AAACTCTTGT AACGTCTTCC

7901   TTTAAGAGCT CTCCTGGCTA GGAGTCACGT AGAAAGGACT ACCGACGAAG
       AAATTCTCGA GAGGACCGAT CCTCAGTGCA TCTTTCCTGA TGGCTGCTTC

7951   GAACTTGGGT CGCCGGTGTG TTCGTATATG GAGGTAGTAA GACCTCCCTT
       CTTGAACCCA GCGGCCACAC AAGCATATAC CTCCATCATT CTGGAGGGAA

8001   TACAACCTAA GGCGAGGAAC TGCCCTTGCT ATTCCACAAT GTCGTCTTAC
       ATGTTGGATT CCGCTCCTTG ACGGGAACGA TAAGGTGTTA CAGCAGAATG

8051   ACCATTGAGT CGTCTCCCCT TTGGAATGGC CCCTGGACCC GGCCCACAAC
       TGGTAACTCA GCAGAGGGGA AACCTTACCG GGGACCTGGG CCGGGTGTTG

8101   CTGGCCCGCT AAGGGAGTCC ATTGTCTGTT ATTTCATGGT CTTTTTACAA
       GACCGGGCGA TTCCCTCAGG TAACAGACAA TAAAGTACCA GAAAAATGTT

8151   ACTCATATAT TTGCTGAGGT TTTGAAGGAT GCGATTAAGG ACCTTGTTAT
       TGAGTATATA AACGACTCCA AAACTTCCTA CGCTAATTCC TGGAACAATA

8201   GACAAAGCCC GCTCCTACCT GCAATATCAG GGTGACTGTG TGCAGCTTTG
       CTGTTTCGGG CGAGGATGGA CGTTATAGTC CCACTGACAC ACGTCGAAAC

8251   ACGATGGAGT AGATTTGCCT CCCTGGTTTC CACCTATGGT GGAAGGGGCT
       TGCTACCTCA TCTAAACGGA GGGACCAAAG GTGGATACCA CCTTCCCCGA

8301   GCCGCGGAGG GTGATGACGG AGATGACGGA GATGAAGGAG GTGATGGAGA
       CGGCGCCTCC CACTACTGCC TCTACTGCCT CTACTTCCTC CACTACCTCT

8351   TGAGGGTGAG GAAGGGCAGG AGTGATGTAA CTTGTTAGGA GACGCCCTCA
       ACTCCCACTC CTTCCCGTCC TCACTACATT GAACAATCCT CTGCGGGAGT

8401   ATCGTATTAA AAGCCGTGTA TTCCCCCGCA CTAAAGAATA AATCCCCAGT
       TAGCATAATT TTCGGCACAT AAGGGGGCGT GATTTCTTAT TTAGGGGTCA

8451   AGACATCATG CGTGCTGTTG GTGTATTTCT GGCCATCTGT CTTGTCACCA
       TCTGTAGTAC GCACGACAAC CACATAAAGA CCGGTAGACA GAACAGTGGT

8501   TTTTCGTCCT CCCAACATGG GGCAATTGGG CATACCCATG TTGTCACGTC
       AAAAGCAGGA GGGTTGTACC CCGTTAACCC GTATGGGTAC AACAGTGCAG

8551   ACTCAGCTCC GCGCTCAACA CCTTCTCGCG TTGGAAAACA TTAGCGACAT
       TGAGTCGAGG CGCGAGTTGT GGAAGAGCGC AACCTTTTGT AATCGCTGTA

8601   TTACCTGGTG AGCAATCAGA CATGCGACGG CTTTAGCCTG GCCTCCTTAA
       AATGGACCAC TCGTTAGTCT GTACGCTGCC GAAATCGGAC CGGAGGAATT
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FIG. 11-9

pCEP4W/hep36

```
8651   ATTCACCTAA GAATGGGAGC AACCAGCATG CAGGAAAAGG ACAAGCAGCG
       TAAGTGGATT CTTACCCTCG TTGGTCGTAC GTCCTTTTCC TGTTCGTCGC
8701   AAAATTCACG CCCCCTTGGG AGGTGGCGGC ATATGCAAAG GATAGCACTC
       TTTTAAGTGC GGGGGAACCC TCCACCGCCG TATACGTTTC CTATCGTGAG
8751   CCACTCTACT ACTGGGTATC ATATGCTGAC TGTATATGCA TGAGGATAGC
       GGTGAGATGA TGACCCATAG TATACGACTG ACATATACGT ACTCCTATCG
8801   ATATGCTACC CGGATACAGA TTAGGATAGC ATATACTACC CAGATATAGA
       TATACGATGG GCCTATGTCT AATCCTATCG TATATGATGG GTCTATATCT
8851   TTAGGATAGC ATATGCTACC CAGATATAGA TTAGGATAGC CTATGCTACC
       AATCCTATCG TATACGATGG GTCTATATCT AATCCTATCG GATACGATGG
8901   CAGATATAAA TTAGGATAGC ATATACTACC CAGATATAGA TTAGGATAGC
       GTCTATATTT AATCCTATCG TATATGATGG GTCTATATCT AATCCTATCG
8951   ATATGCTACC CAGATATAGA TTAGGATAGC CTATGCTACC CAGATATAGA
       TATACGATGG GTCTATATCT AATCCTATCG GATACGATGG GTCTATATCT
9001   TTAGGATAGC ATATGCTACC CAGATATAGA TTAGGATAGC ATATGCTATC
       AATCCTATCG TATACGATGG GTCTATATCT AATCCTATCG TATACGATAG
9051   CAGATATTTG GGTAGTATAT GCTACCCAGA TATAAATTAG GATAGCATAT
       GTCTATAAAC CCATCATATA CGATGGGTCT ATATTAATC CTATCGTATA
9101   ACTACCCTAA TCTCTATTAG GATAGCATAT GCTACCCGGA TACAGATTAG
       TGATGGGATT AGAGATAATC CTATCGTATA CGATGGGCCT ATGTCTAATC
9151   GATAGCATAT ACTACCCAGA TATAGATTAG GATAGCATAT GCTACCCAGA
       CTATCGTATA TGATGGGTCT ATATCTAATC CTATCGTATA CGATGGGTCT
9201   TATAGATTAG GATAGCCTAT GCTACCCAGA TATAAATTAG GATAGCATAT
       ATATCTAATC CTATCGGATA CGATGGGTCT ATATTAATC CTATCGTATA
9251   ACTACCCAGA TATAGATTAG GATAGCATAT GCTACCCAGA TATAGATTAG
       TGATGGGTCT ATATCTAATC CTATCGTATA CGATGGGTCT ATATCTAATC
9301   GATAGCCTAT GCTACCCAGA TATAGATTAG GATAGCATAT GCTATCCAGA
       CTATCGGATA CGATGGGTCT ATATCTAATC CTATCGTATA CGATAGGTCT
9351   TATTTGGGTA GTATATGCTA CCCATGGCAA CATTAGCCCA CCGTGCTCTC
       ATAAACCCAT CATATACGAT GGGTACCGTT GTAATCGGGT GGCACGAGAG
9401   AGCGACCTCG TGAATATGAG GACCAACAAC CCTGTGCTTG GCGCTCAGGC
       TCGCTGGAGC ACTTATACTC CTGGTTGTTG GGACACGAAC CGCGAGTCCG
9451   GCAAGTGTGT GTAATTTGTC CTCCAGATCG CAGCAATCGC GCCCCTATCT
       CGTTCACACA CATTAAACAG GAGGTCTAGC GTCGTTAGCG CGGGGATAGA
9501   TGGCCCGCCC ACCTACTTAT GCAGGTATTC CCCGGGGTGC CATTAGTGGT
       ACCGGGCGGG TGGATGAATA CGTCCATAAG GGGCCCCACG GTAATCACCA
9551   TTTGTGGGCA AGTGGTTTGA CCGCAGTGGT TAGCGGGGTT ACAATCAGCC
       AAACACCCGT TCACCAAACT GGCGTCACCA ATCGCCCCAA TGTTAGTCGG
9601   AAGTTATTAC ACCCTTATTT TACAGTCCAA AACCGCAGGG CGGCGTGTGG
       TTCAATAATG TGGGAATAAA ATGTCAGGTT TTGGCGTCCC GCCGCACACC
9651   GGGCTGACGC GTGCCCCAC TCCACAATTT CAAAAAAAAG AGTGGCCACT
       CCCGACTGCG CACGGGGGTG AGGTGTTAAA GTTTTTTTTC TCACCGGTGA
9701   TGTCTTTGTT TATGGCCCC ATTGGCGTGG AGCCCCGTTT AATTTTCGGG
       ACAGAAACAA ATACCCGGGG TAACCGCACC TCGGGCAAA TTAAAAGCCC
9751   GGTGTTAGAG ACAACCAGTG GAGTCCGCTG CTGTCGGCGT CCACTCTCTT
       CCACAATCTC TGTTGGTCAC CTCAGGCGAC GACAGCCGCA GGTGAGAGAA
```

FIG. 11-10

pCEP4W/hep36

```
 9801   TCCCCTTGTT ACAAATAGAG TGTAACAACA TGGTTCACCT GTCTTGGTCC
        AGGGGAACAA TGTTTATCTC ACATTGTTGT ACCAAGTGGA CAGAACCAGG
 9851   CTGCCTGGGA CACATCTTAA TAACCCCAGT ATCATATTGC ACTAGGATTA
        GACGGACCCT GTGTAGAATT ATTGGGGTCA TAGTATAACG TGATCCTAAT
 9901   TGTGTTGCCC ATAGCCATAA ATTCGTGTGA GATGGACATC CAGTCTTTAC
        ACACAACGGG TATCGGTATT TAAGCACACT CTACCTGTAG GTCAGAAATG
 9951   GGCTTGTCCC CACCCCATGG ATTTCTATTG TTAAAGATAT TCAGAATGTT
        CCGAACAGGG GTGGGGTACC TAAAGATAAC AATTTCTATA AGTCTTACAA
10001   TCATTCCTAC ACTAGTATTT ATTGCCCAAG GGGTTTGTGA GGGTTATATT
        AGTAAGGATG TGATCATAAA TAACGGGTTC CCCAAACACT CCCAATATAA
10051   GGTGTCATAG CACAATGCCA CCACTGAACC CCCCGTCCAA ATTTTATTCT
        CCACAGTATC GTGTTACGGT GGTGACTTGG GGGGCAGGTT TAAAATAAGA
10101   GGGGGCGTCA CCTGAAACCT TGTTTTCGAG CACCTCACAT ACACCTTACT
        CCCCCGCAGT GGACTTTGGA ACAAAAGCTC GTGGAGTGTA TGTGGAATGA
10151   GTTCACAACT CAGCAGTTAT TCTATTAGCT AAACGAAGGA GAATGAAGAA
        CAAGTGTTGA GTCGTCAATA AGATAATCGA TTTGCTTCCT CTTACTTCTT
10201   GCAGGCGAAG ATTCAGGAGA GTTCACTGCC CGCTCCTTGA TCTTCAGCCA
        CGTCCGCTTC TAAGTCCTCT CAAGTGACGG GCGAGGAACT AGAAGTCGGT
10251   CTGCCCTTGT GACTAAAATG GTTCACTACC CTCGTGGAAT CCTGACCCCA
        GACGGGAACA CTGATTTTAC CAAGTGATGG GAGCACCTTA GGACTGGGGT
10301   TGTAAATAAA ACCGTGACAG CTCATGGGGT GGGAGATATC GCTGTTCCTT
        ACATTTATTT TGGCACTGTC GAGTACCCCA CCCTCTATAG CGACAAGGAA
10351   AGGACCCTTT TACTAACCCT AATTCGATAG CATATGCTTC CCGTTGGGTA
        TCCTGGGAAA ATGATTGGGA TTAAGCTATC GTATACGAAG GGCAACCCAT
10401   ACATATGCTA TTGAATTAGG GTTAGTCTGG ATAGTATATA CTACTACCCG
        TGTATACGAT AACTTAATCC CAATCAGACC TATCATATAT GATGATGGGC
10451   GGAAGCATAT GCTACCCGTT TAGGGTTAAC AAGGGGGCCT TATAAACACT
        CCTTCGTATA CGATGGGCAA ATCCCAATTG TTCCCCCGGA ATATTTGTGA
10501   ATTGCTAATG CCCTCTTGAG GGTCCGCTTA TCGGTAGCTA CACAGGCCCC
        TAACGATTAC GGGAGAACTC CCAGGCGAAT AGCCATCGAT GTGTCCGGGG
10551   TCTGATTGAC GTTGGTGTAG CCTCCCGTAG TCTTCCTGGG CCCCTGGGAG
        AGACTAACTG CAACCACATC GGAGGGCATC AGAAGGACCC GGGGACCCTC
10601   GTACATGTCC CCCAGCATTG GTGTAAGAGC TTCAGCCAAG AGTTACACAT
        CATGTACAGG GGGTCGTAAC CACATTCTCG AAGTCGGTTC TCAATGTGTA
10651   AAAGGCAATG TTGTGTTGCA GTCCACAGAC TGCAAAGTCT GCTCCAGGAT
        TTTCCGTTAC AACACAACGT CAGGTGTCTG ACGTTTCAGA CGAGGTCCTA
10701   GAAAGCCACT CAGTGTTGGC AAATGTGCAC ATCCATTTAT AAGGATGTCA
        CTTTCGGTGA GTCACAACCG TTTACACGTG TAGGTAAATA TTCCTACAGT
10751   ACTACAGTCA GAGAACCCCT TTGTGTTTGG TCCCCCCCCG TGTCACATGT
        TGATGTCAGT CTCTTGGGGA AACACAAACC AGGGGGGGGC ACAGTGTACA
10801   GGAACAGGGC CCAGTTGGCA AGTTGTACCA ACCAACTGAA GGGATTACAT
        CCTTGTCCCG GGTCAACCGT TCAACATGGT TGGTTGACTT CCCTAATGTA
10851   GCACTGCCCC GCGAAGAAGG GGCAGAGATG CCGTAGTCAG GTTTAGTTCG
        CGTGACGGGG CGCTTCTTCC CCGTCTCTAC GGCATCAGTC CAAATCAAGC
10901   TCCGGCGGCG GGGCTCTAGA GTCGACCGGT CATGGCTGCG CCCCGACACC
        AGGCCGCCGC CCCGAGATCT CAGCTGGCCA GTACCGACGC GGGGCTGTGG
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FIG. 11-11

pCEP4W/hep36

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10951  CGCCAACACC  CGCTGACGCG  CCCTGACGGG  CTTGTCTGCT  CCCGGCATCC
       GCGGTTGTGG  GCGACTGCGC  GGGACTGCCC  GAACAGACGA  GGGCCGTAGG
11001  GCTTACAGAC  AAGCTGTGAC  CGTCTCCGGG  AGCTGCATGT  GTCAGAGGTT
       CGAATGTCTG  TTCGACACTG  GCAGAGGCCC  TCGACGTACA  CAGTCTCCAA
11051  TTCACCGTCA  TCACCGAAAC  GCGCGAGGCA  GCCGGATCAT  AATCAGCCAT
       AAGTGGCAGT  AGTGGCTTTG  CGCGCTCCGT  CGGCCTAGTA  TTAGTCGGTA
11101  ACCACATTTG  TAGAGGTTTT  ACTTGCTTTA  AAAAACCTCC  CCACCTCCCC
       TGGTGTAAAC  ATCTCCAAAA  TGAACGAAAT  TTTTTGGAGG  GGTGGAGGGG
11151  CTGAACCTGA  AACATAAAAT  GAATGCAATT  GTTGTTGTTA  ACTTGTTTAT
       GACTTGGACT  TTGTATTTTA  CTTACGTTAA  CAACAACAAT  TGAACAAATA
11201  TGCAGCTTAT  AATGGTTACA  AATAAAGCAA  TAGCATCACA  AATTTCACAA
       ACGTCGAATA  TTACCAATGT  TTATTTCGTT  ATCGTAGTGT  TTAAAGTGTT
11251  ATAAAGCATT  TTTTTCACTG  CATTCTAGTT  GTGGTTTGTC  CAAACTCATC
       TATTTCGTAA  AAAAAGTGAC  GTAAGATCAA  CACCAAACAG  GTTTGAGTAG
11301  AATGTATCTT  ATCATGTCTG  GATCCCACGT  GCAGGCGGGG  AGGCGGCCCA
       TTACATAGAA  TAGTACAGAC  CTAGGGTGCA  CGTCCGCCCC  TCCGCCGGGT
11351  AAGGGAGATC  CGACTCGTCT  GAGGGCGAAG  GCGAAGACGC  GGAAGAGGCC
       TTCCCTCTAG  GCTGAGCAGA  CTCCCGCTTC  CGCTTCTGCG  CCTTCTCCGG
11401  GCAGAGCCGG  CAGCAGGCCG  CGGGAAGGAA  GGTCCGCTGG  ATTGAGGGCC
       CGTCTCGGCC  GTCGTCCGGC  GCCCTTCCTT  CCAGGCGACC  TAACTCCCGG
11451  GAAGGGACGT  AGCAGAAGGA  CGTCCCGCGC  AGAATCCAGG  TGGCAACACA
       CTTCCCTGCA  TCGTCTTCCT  GCAGGGCGCG  TCTTAGGTCC  ACCGTTGTGT
11501  GGCGAGCAGC  CAAGGAAAGG  ACGATGATTT  CCCCGACAAC  ACCACGGAAT
       CCGCTCGTCG  GTTCCTTTCC  TGCTACTAAA  GGGGCTGTTG  TGGTGCCTTA
11551  TGTCAGTGCC  CAACAGCCGA  GCCCCTGTCC  AGCAGCGGGC  AAGGCAGGCG
       ACAGTCACGG  GTTGTCGGCT  CGGGGACAGG  TCGTCGCCCG  TTCCGTCCGC
11601  GCGATGAGTT  CCGCCGTGGC  AATAGGGAGG  GGGAAAGCGA  AAGTCCCGGA
       CGCTACTCAA  GGCGGCACCG  TTATCCCTCC  CCCTTTCGCT  TTCAGGGCCT
11651  AAGGAGCTGA  CAGGTGGTGG  CAATGCCCCA  ACCAGTGGGG  GTTGCGTCAG
       TTCCTCGACT  GTCCACCACC  GTTACGGGGT  TGGTCACCCC  CAACGCAGTC
11701  CAAACACAGT  GCACCACG  CCACGTTGCC  TGACAACGGG  CCACAACTCC
       GTTTGTGTCA  CGTGTGGTGC  GGTGCAACGG  ACTGTTGCCC  GGTGTTGAGG
11751  TCATAAAGAG  ACAGCAACCA  GGATTTATAC  AAGGAGGAGA  AAATGAAAGC
       AGTATTTCTC  TGTCGTTGGT  CCTAAATATG  TTCCTCCTCT  TTTACTTTCG
11801  CATACGGGAA  GCAATAGCAT  GATACAAAGG  CATTAAAGCA  GCGTATCCAC
       GTATGCCCTT  CGTTATCGTA  CTATGTTTCC  GTAATTTCGT  CGCATAGGTG
11851  ATAGCGTAAA  AGGAGCAACA  TAGTTAAGAA  TACCAGTCAA  TCTTTCACAA
       TATCGCATTT  TCCTCGTTGT  ATCAATTCTT  ATGGTCAGTT  AGAAAGTGTT
11901  ATTTTGTAAT  CCAGAGGTTG  ATTC
       TAAAACATTA  GGTCTCCAAC  TAAG
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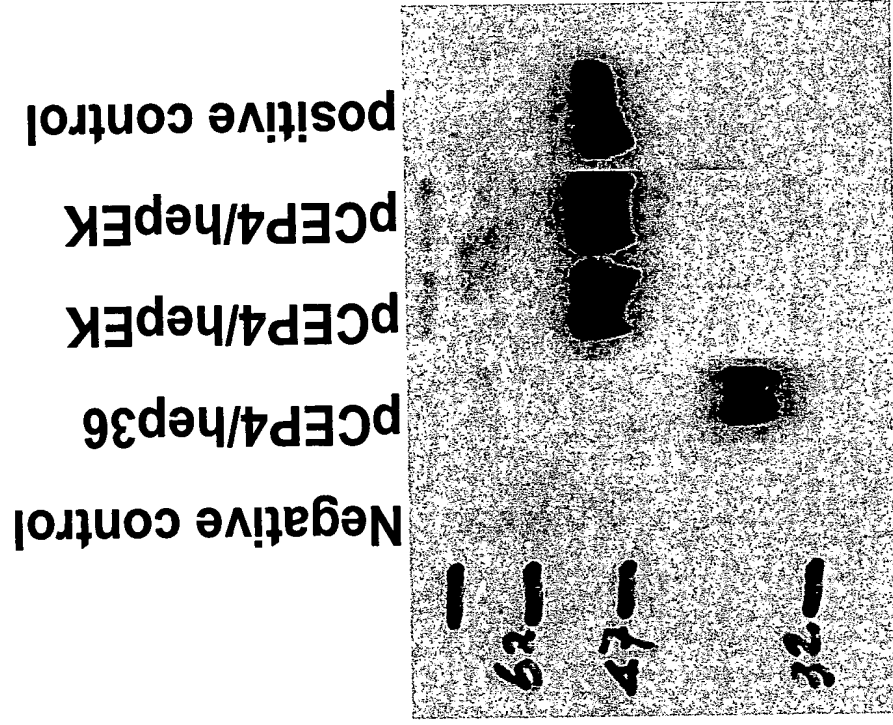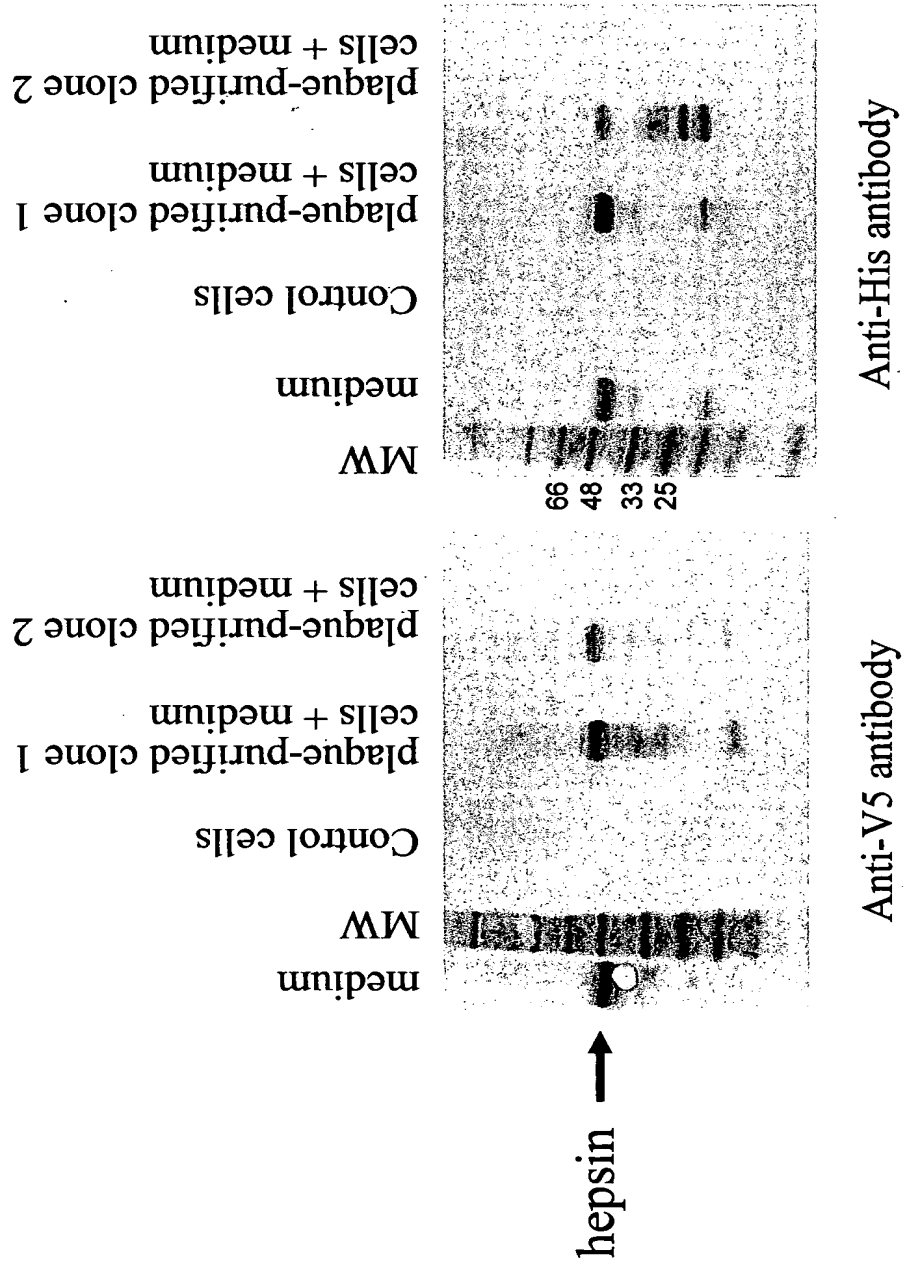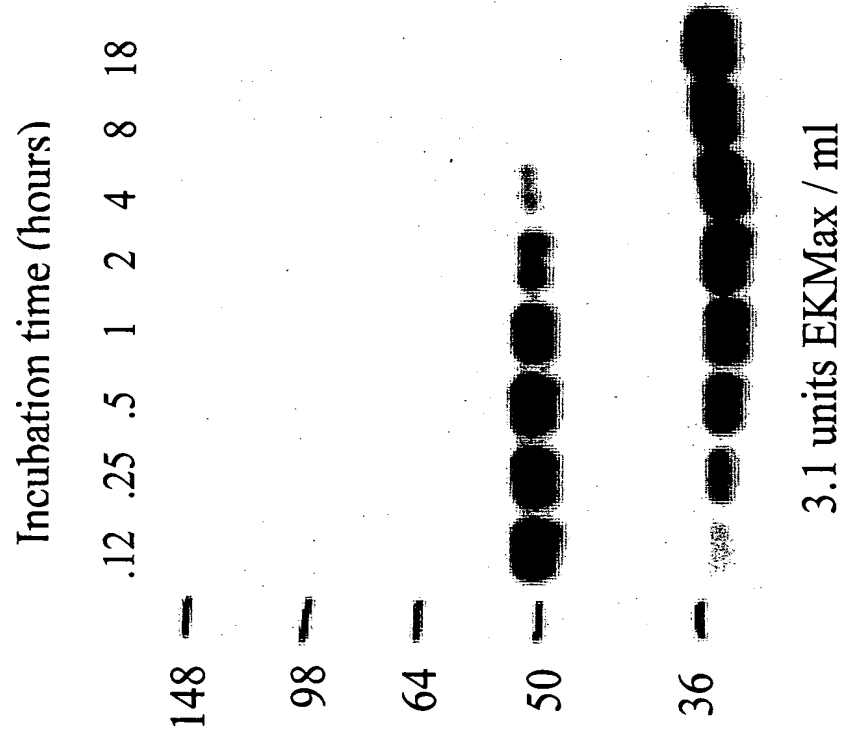
FIG. 12

FIG. 13

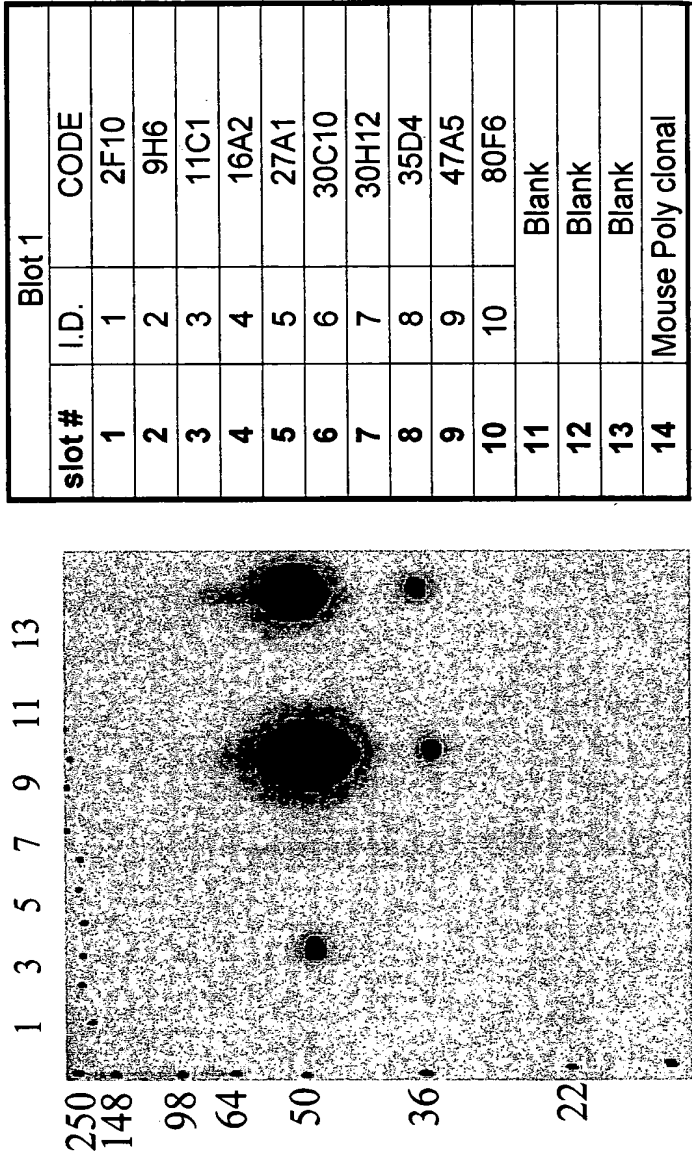Anti-V5 antibody

medium
MW
Control cells
plague-purified clone 1
cells + medium
plague-purified clone 2
cells + medium

hepsin

Anti-His antibody

MW
medium
Control cells
plague-purified clone 1
cells + medium
plague-purified clone 2
cells + medium

66
48
33
25

FIG. 14

FIG. 15A

slot #	I.D.	Blot 1	
		CODE	
1	1	2F10	
2	2	9H6	
3	3	11C1	
4	4	16A2	
5	5	27A1	
6	6	30C10	
7	7	30H12	
8	8	35D4	
9	9	47A5	
10	10	80F6	
11		Blank	
12		Blank	
13		Blank	
14		Mouse Poly clonal	

FIG. 15B

Blot 1		
slot #	I.D.	CODE
1	1	7H3
2	2	12A2
3	3	16A3
4	4	20D1
5	5	22A3
6	6	31C1
7	7	31H2
8	8	36B2
9	9	38 E2
10	10	39D6
11	11	41F7
12	12	42 E3
13	Blank	
14		Mouse Poly clonal

FIG. 15C
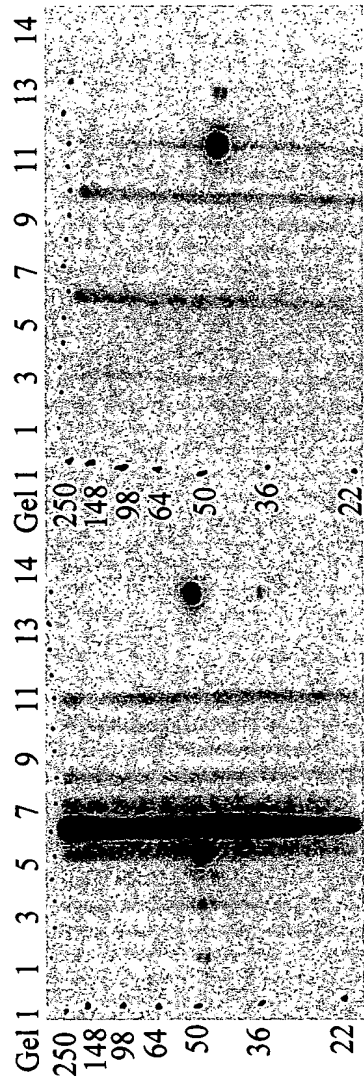
Gel 1

Slot	Sample	Dilution
1	Rabbit Polyclonal –Cayman Chem	1:500
2	Media	neat
3	37G10	"
4	94A7	"
5	46D12	"
6	103E3	"
7	40F1	"
8	103H12	"
9	93D1	"
10	10C2	"
11	102F2	"
12	83E11	"
13	Blank	
14	Blank	
15	Protein - ♂ mouse	1:5000

Gel 2

Slot	Sample	Dilution
1	Protein - ♂ mouse	1:5000
2	Media	neat
3	27E7	"
4	92A7	"
5	91A4	"
6	99B11	"
7	94C7	"
8	91A1	"
9	14H11	"
10	74C7	"
11	72H6	"
12	14C7	"
13	Blank	.
14	Rabbit Polyclonal –Cayman Chem	1:500
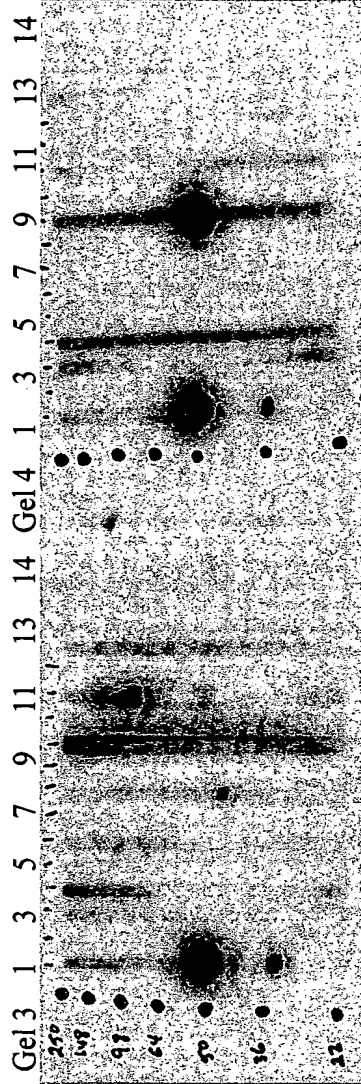
FIG. 15D

Gel 3

Slot	Sample	Dilution
1	Protein - ♂ mouse	1:5000
2	Media	neat
3	84G6	"
4	84H2	"
5	51F8	"
6	15b11	"
7	90E6	"
8	72H6	"
9	85A4	"
10	87C2	"
11	3G11	"
12	53E11	"
13	91H4	"
14	53C7	"
15	88C7	"

Gel 4

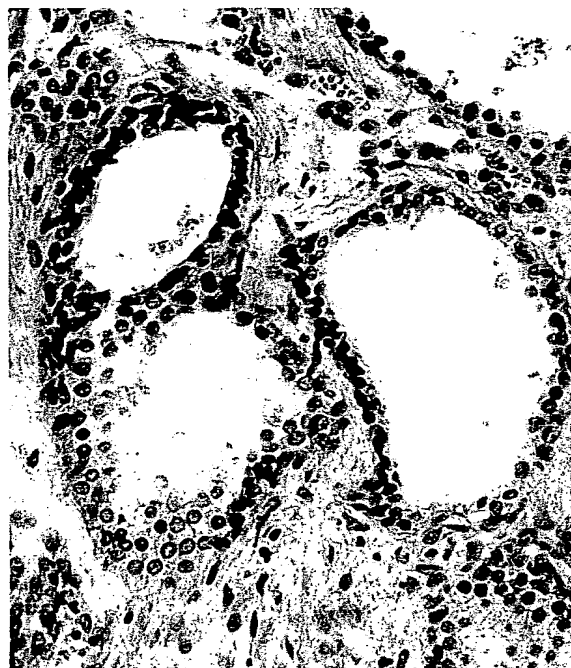| Slot	Sample	Dilution
1	Protein - ♂ mouse	1:5000
2	Media	neat
3	75H3	"
4	98B4	"
5	91C9	"
6	53D9	"
7	80G6	"
8	95F3	"
9	14C7	"
10	80H10	"
11	92A9	"
12	81C8	"
13	96B6	"
14	18I2	"

FIG. 16A
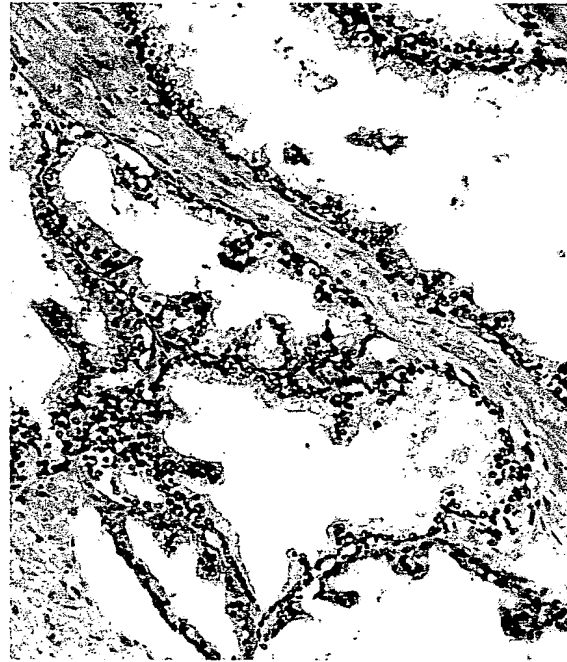
Control
Anti-Hepsin mouse
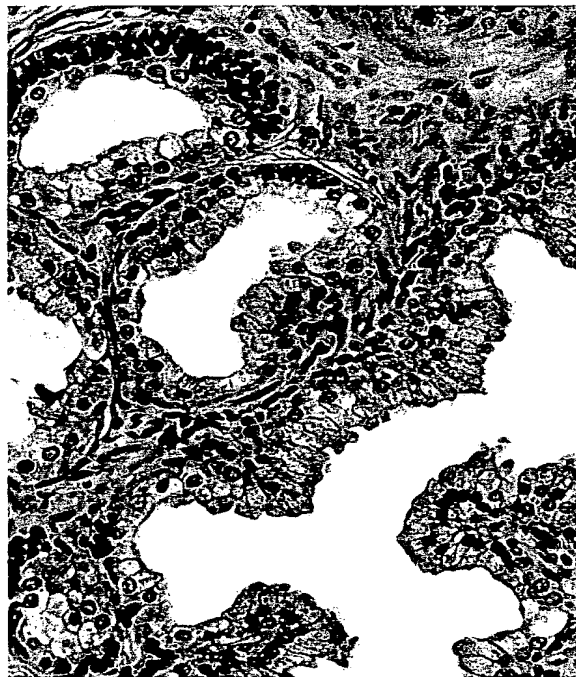polyclonal preimmun
1/500 (9)
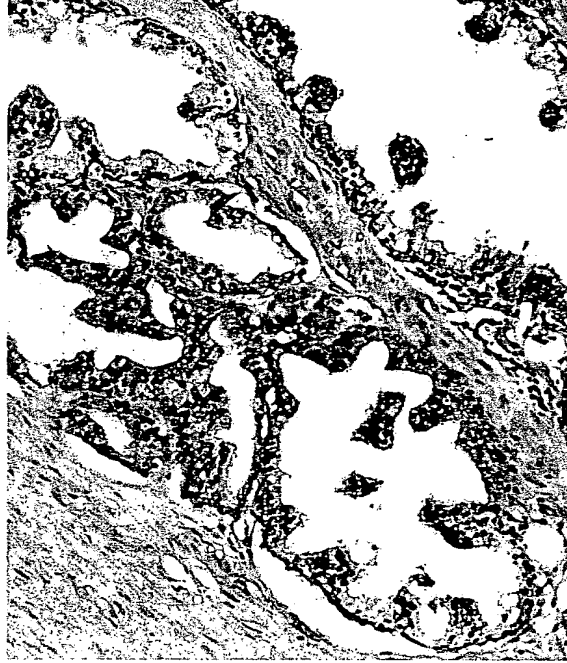
Anti-Hepsin mouse
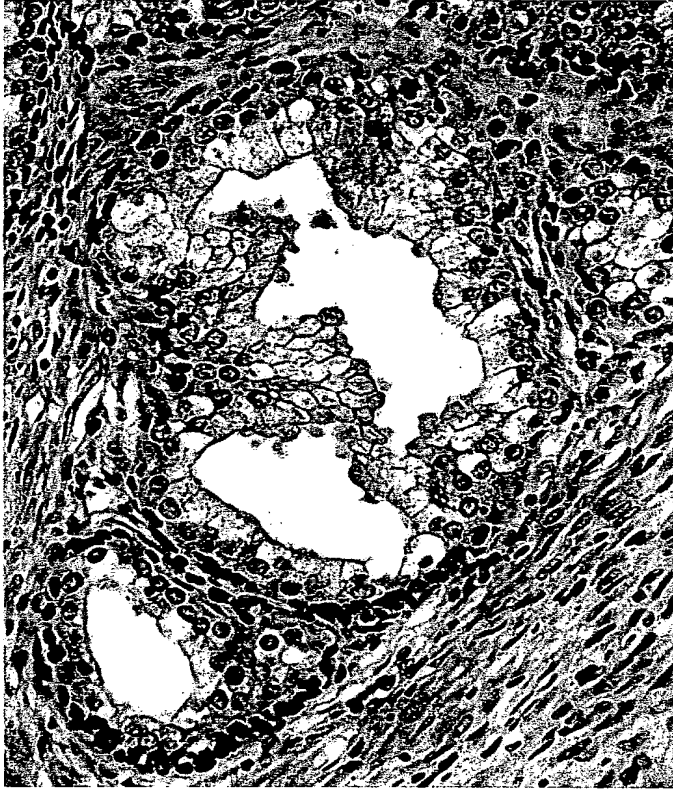polyclonal immun
1/500 (10)

FIG. 16B

Control medium

Anti-Hepsin monoclonal ab (medium)

FIG. 16C

Anti-Hepsin monoclonal ab

FIG. 17

Human wild-type hepsin amino acid sequence:

```
maqkeggrtv pccsrpkvaa ltagtlllt aigaaswaiv avllrsdqep lypvqvssad  61
arlmvfdkte gtwrllcssr snarvaglsc eemgflralt hseldvrtag angtsgffcv  121
degrlphtqr llevisvcdc prgrflaaic qdcgrrklpv drivggrdts lgrwpwqvsl  181
rydgahlcgg sllsgdwvlt aahcfpernr vlsrwrvfag avaqasphgl qlgvqavvyh  241
ggylpfrdpn seensndial vhlsspplt eyiqpvclpa agqalvdgki ctvtgwgntq  301
yygqagvlq earvpiisnd vcngadfygn qikpkmfcag qikpkmfcag ypeggidacq gdsggpfvce  361
dsisrtprwr lcgivswgtg calaqkpgvy tkvsdfrewi fqaikthsea sgmvtql
```

the cytoplasmic domain: Met1 to Lys17
the transmembrane domain: Val18 to Leu44
the ectodomain: Arg45 to Leu417

FIG. 18

Hep-ED-EK structure (modified soluble hepsin with substitute activation sequence)

```
  1 RSDQEPLYPV QVSSADARLM VFDKTEGTWR LLCSSRSNAR VAGLSCEEMG FLRALTHSEL
 61 DVRTAGANGT SGFFCVDEGR LPHTQRLLEV ISVCDCPRGR FLAAICQDCG RRKLPVDDDD
121 KIVGGRDTSL GRWPWQVSLR YDGAHLCGGS LLSGDWVLTA AHCFPERNRV LSRWRVFAGA
181 VAQASPHGLQ LGVQAVVYHG GYLPFRDPNS EENSNDIALV HLSSPLPLTE YIQPVCLPAA
241 GQALVDGKIC TVTGWGNTQY YGQQAGVLQE ARVPIISNDV CNGADFYGNQ IKPKMFCAGY
301 PEGGIDACQG DSGGPFVCED SISRTPRWRL CGIVSWGTGC ALAQKPGVYT KVSDFREWIF
361 QAIKTHSEAS GMVTQLEFGK PIPNPLLGLD STRTGHHHHH H*
```

Cytoplasmic domain: absent
Transmembrane domain: absent
Modified activation domain:117-121 (underlined)
V5 and 6-His Tag: 377-401

FIG.19

Antibody Neutralization

Relative Rate %

■ Hepsin tf BHK ▩ Hepsin tf BHK no F7 ▨ BHK parental